

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 09:22:18 ; Search time 165 Seconds
(without alignments)
480,520 Million cell updates/sec

Title: US-10-087-190-3

Perfect score: 1047
Sequence: 1 MSKKKGLSAEKRTIMEIF.....FEENKIDRTFGIPEDFYID 205

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047	100.0	205	7	ADD84537 121P1.P
2	1047	100.0	205	7	ADJ70015 Human hea
3	1047	100.0	205	8	ADM83851 Human can
4	1047	100.0	205	8	ADM83810 Human can
5	1047	100.0	205	8	ADM83812 Human can
6	1047	100.0	205	8	ADM83793 Human can
7	1047	100.0	205	8	ADM83811 Human can
8	1047	100.0	205	8	ADM83804 Human can
9	1047	100.0	219	6	ABP75541 Human sec
10	1036.5	99.0	206	8	ADM83834 Human can
11	1036.5	99.0	206	8	ADM83835 Human can
12	1011	96.6	198	8	ADM83814 Human can
13	975	93.1	190	4	AAM40043 Human pol
14	975	93.1	190	7	ADD84547 121P1.V
15	975	93.1	190	8	ADM83857 Human can
16	975	93.1	190	8	ADM83859 Human can
17	975	93.1	190	8	ADM83803 Human can
18	975	93.1	190	8	ADM83809 Human can
19	975	93.1	190	8	ADM83858 Human can
20	948	90.5	205	8	ADM83813 Mouse hyp
21	945.5	90.3	190	7	ADD84545 121P1.V
22	945.5	90.3	190	8	ADM83808 Human can
23	945.5	90.3	190	8	ADM83801 Human can
24	945.5	90.3	190	8	ADM83853 Human can
25	945.5	90.3	190	8	ADM83852 Human can

26	614	58.6	122	8	ADM83843 Human can
27	606	57.9	122	4	AAM41829 Human pol
28	591	56.4	122	7	ADD84543 121P1.V
29	591	56.4	122	8	ADM83799 Human can
30	591	56.4	122	8	ADM83845 Human can
31	591	56.4	122	8	ADM83807 Human can
32	591	56.4	122	8	ADM83844 Human can
33	584	55.8	119	7	ADD84541 121P1.V
34	584	55.8	119	8	ADM83806 Human can
35	584	55.8	119	8	ADM83837 Human can
36	584	55.8	119	7	ADD84539 121P1.V
37	465	44.4	126	8	ADM83836 Human can
38	465	44.4	126	8	ADM83795 Human can
39	465	44.4	126	8	ADM83805 Human can
40	465	44.4	126	8	ADM83815 Yeast hyp
41	349	33.3	200	8	ABG12341 Novel hum
42	329.5	31.5	182	4	ABG74669 Human col
43	287	27.4	218	5	ADH32846 Yeast smo
44	255.5	24.4	218	5	ADP26646 Mouse dyn
45	135.5	12.9	1281	8	

ALIGNMENTS

RESULT 1	
ID	ADD84537 standard; protein; 205 AA.
AC	ADD84537;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	121P1 protein.
XX	
KW	121P1; 121P1 modulation; human; chromosome 4q; cytostatic;
XX	gene therapy; vaccine; cancer; immune response; immunisation.
OS	Homo sapiens.
XX	
PN	WO200295009-A2.
XX	
PD	28-NOV-2002.
XX	
PF	28-FEB-2002; 2002MO-US006242.
XX	
PR	05-MAR-2001; 2001US-00799250.
XX	
PA	(AGEN-) AGENSYS INC.
XX	
PI	Challita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
XX	Jakobovits A;
PI	WPI; 2003-156757/15.
XX	N-PSDB; ADD84536.
DR	
PT	Composition comprising a substance that modulates the status of 121P1,
XX	useful in diagnosing, preventing, prognosticating or treating patients
PT	with cancer that expresses 121P1, such as breast, colon, ovarian or
XX	lung cancer.
PS	Claim 19; Fig 2A; 285pp; English.
XX	
CC	The present invention describes a composition (I) comprising a substance
XX	that modulates the status of 121P1 (gene and encoded protein), or a
CC	molecule that is modulated by 121P1, where the status of a cell that
XX	expresses 121P1 is modulated. The human 121P1 gene maps to chromosome
CC	4q. (I) has cytostatic activity, and can be used in gene therapy, and in
XX	vaccines. The composition (I) can be used for diagnosing, preventing,
CC	prognosticating or treating patients with cancer that expresses 121P1,
XX	such as breast, colon, ovarian or lung cancer. The 121P1 gene or its
CC	fragment can be used to elicit a humoral or cellular immune response.
XX	121P1 antibodies can be used in active or passive immunisation. 121P1

CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121P1F1 genes, as coding sequences for directing the
CC expression of 121P1F1 polypeptides, or as tools for modulating or
CC inhibiting the expression of 121P1F1 genes. The present sequence is used
CC in the exemplification of the present invention.

XX
SQ Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 7; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEKKRTMMEIFSETKDVFOUKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
DB 1 MSKKKGLSAEKKRTMMEIFSETKDVFOUKDLKIAPEKGITAMSVKVLQSLVDDGMV 60

QY 61 DCEIRIGTSNYWAFPSKALHARKHKLVLVLSQSLSGSKHSLQKSIIEKAKIGRCETERR 120
DB 61 DCEIRIGTSNYWAFPSKALHARKHKLVLVLSQSLSGSKHSLQKSIIEKAKIGRCETERR 120

QY 121 TRIAKEISSLRDQREQLKAEVEKXKDCDPQVVEIRQANKVAKKANRWTDNI FAKISWA 180
DB 121 TRIAKEISSLRDQREQLKAEVEKXKDCDPQVVEIRQANKVAKKANRWTDNI FAKISWA 180

QY 181 KRRFGPEENKIDRTFGIPEDFDYID 205
DB 181 KRRFGPEENKIDRTFGIPEDFDYID 205

RESULT 2
ADJ70015
ID ADJ70015 standard; protein; 205 AA.

AC ADJ70015;
XX
XX 06-MAY-2004 (first entry)

DE Human heart mitochondrial protein as a therapeutic target SeqID1821.

XX
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
XX Huntington's disease; osteoarthritis;
XX Leber's hereditary optic neuropathy; LHON;
XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
XX osteopathic; ophthalmological; cytoskeletal.

OS Homo sapiens.
XX
XX
XX WO2003087768-A2.

XX
XX 23-OCT-2003.
XX
XX
XX 04-APR-2003; 2003WO-US010870.

XX
XX
XX 12-APR-2002; 2002US-0372843P.
XX 17-JUN-2002; 2002US-0389987P.
XX 20-SEP-2002; 2002US-0412418P.

XX
XX
XX (MITO-) MITOKOR.
XX (BUCK-) BUCK INST AGE RES.

XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
XX Warnock DE;
XX
XX WPI; 2003-845369/78.

XX
XX Identifying a mitochondrial target for drug screening assays and for
XX treating diseases associated with altered mitochondrial function,
XX comprises detecting a modified polypeptide in a sample and correlating
XX with the disease.

XX
XX Claim 1, SEQ ID NO 1821; 180pp; English.

XX
XX This invention relates to novel mitochondrial targets that can be used
XX for therapeutic intervention in treating a disease associated with
XX altered mitochondrial function. Specifically, it refers to a method for
XX identifying proteins of the human heart mitochondrial proteome that are
XX useful for drug screening assays, as well as therapeutic targets. The
XX present invention describes a method for identifying such proteins that
XX can be used in the treatment of various diseases associated with altered
XX mitochondrial function including diabetes mellitus, Huntington's disease,
XX osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX compositions have neuroprotective, neurotropic, antidiabetic,
XX anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX cytoskeletal activities. This polypeptide sequence is a human heart
XX mitochondrial protein of the invention.

XX
SQ Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 7; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEKKRTMMEIFSETKDVFOUKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
DB 1 MSKKKGLSAEKKRTMMEIFSETKDVFOUKDLKIAPEKGITAMSVKVLQSLVDDGMV 60

QY 61 DCEIRIGTSNYWAFPSKALHARKHKLVLVLSQSLSGSKHSLQKSIIEKAKIGRCETERR 120
DB 61 DCEIRIGTSNYWAFPSKALHARKHKLVLVLSQSLSGSKHSLQKSIIEKAKIGRCETERR 120

QY 121 TRIAKEISSLRDQREQLKAEVEKXKDCDPQVVEIRQANKVAKKANRWTDNI FAKISWA 180
DB 121 TRIAKEISSLRDQREQLKAEVEKXKDCDPQVVEIRQANKVAKKANRWTDNI FAKISWA 180

QY 181 KRRFGPEENKIDRTFGIPEDFDYID 205
DB 181 KRRFGPEENKIDRTFGIPEDFDYID 205

RESULT 3
ADM83851
ID ADM83851 standard; protein; 205 AA.

AC ADM83851;
XX
XX
XX 03-JUN-2004 (first entry)

DE Human cancer gene 121P1F1 protein #6.

XX
XX
XX Human; cancer gene 121P1F1; cytoskeletal; cancer; chromosome 4q; HLA;
XX human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
XX colon cancer; lung cancer; pancreatic cancer; breast cancer;
XX cervical cancer; stomach cancer; gene therapy; vaccine.

OS Homo sapiens.
XX
XX
XX US2003223997-A1.

XX
XX
XX 04-DEC-2003.
XX
XX 28-FEB-2002; 2002US-00087190.
XX 08-FEB-2001; 2001US-00779250.

XX
XX
XX (CHAL/) CHALLITA-BID P M.
XX (HUBER/) HUBERT R S.
XX (RAIT/) RAITANO A B.
XX (FARI/) FARIS M.
XX (AFAR/) AFAR D E H.
XX (GEMW/) GE W.
XX (JAKO/) JAKOBOVITS A.

PI Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;
XX
XX WPI; 2004-060522/06.

PT New composition comprising a substance that modulates the status of
PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.

XX Example 5; SEQ ID NO 61; 211pp; English.

XX The invention relates to a composition comprising a substance that
XX modulates the status of 121P1F1 (a protein encoded by a cancer expressed
XX gene) or a molecule that is modulated by 121P1F1 where status of the cell
XX that expresses 121P1F1 is modulated. Also included are a pharmaceutical
XX composition comprising the novel composition in a human unit dose form, a
XX recombinant protein comprising an antigen-binding region of a monoclonal
XX antibody, a non-human transgenic animal that produces an antibody, a
XX hybridoma that produces an antibody, a single chain monoclonal antibody
XX that immunospecifically binds to a 121P1F1-related protein (comprising
XX the variable domains of the heavy and light chains of a monoclonal
XX antibody), a vector comprising a polynucleotide that encodes a single
XX chain monoclonal antibody, a polynucleotide that encodes an analogue
XX peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
XX that expresses 121P1F1, inhibiting growth of cancer cells that expresses
XX 121P1F1 (comprising administering to the cells the composition), treating
XX a patient who bears cancer cells that express 121P1F1, generating a
XX mammalian immune response directed to 121P1F1, inducing an immune
XX response, monitoring 121P1F1 gene products in a biological sample from a
XX patient who has or who is suspected of having cancer, monitoring the
XX presence of cancer in an individual and an assay for detecting the
XX presence of a 121P1F1-related protein or polynucleotide in a biological
XX sample from a patient who has or who is suspected of having cancer. The
XX composition may comprise a polynucleotide that comprises a 121P1F1-
XX related protein coding sequence provided that the coding sequence does
XX not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
XX substance also comprises a polynucleotide that encodes at least one
XX peptide given in 16 Tables (given in the specification), the peptides
XX being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
XX splice variants. The composition is useful for detecting, treating or
XX preventing cancer, preferably prostate cancer, bladder cancer, kidney
XX cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
XX cervical cancer or stomach cancer. The composition can also be used as a
XX vaccine to treat or prevent cancer that expresses or overexpresses
XX 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
XX sequence is a 121P1F1 protein (full-length or fragment).

XX Sequence 205 AA;

XX Query Match 100.0%; Score 1047; DB 8; Length 205;

XX Best Local Similarity 100.0%; Pred. No. 1.5e-88;
XX Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKGSLAEKRTMWEIFSETKOVFOIKDLEKTAPEKKGTTAMSVKVLDSIVDDGV 60
DB 1 MSKKGSLAEKRTMWEIFSETKOVFOIKDLEKTAPEKKGTTAMSVKVLDSIVDDGV 60
QY 61 DERICTSNVYVAFPSKALHARKKLEVESQLSSEGSQKASLOKSIERAKIGRCETTER 120
DB 61 DERICTSNVYVAFPSKALHARKKLEVESQLSSEGSQKASLOKSIERAKIGRCETTER 120
QY 121 TRLAKELSLRDQREOLKAVERKXKCDPVVEEIRQANKVAKAANRWTDNIPAIKSWA 180
DB 121 TRLAKELSLRDQREOLKAVERKXKCDPVVEEIRQANKVAKAANRWTDNIPAIKSWA 180
QY 181 KKKFGFEENKIDRTFGIPEDFDYID 205
DB 181 KKKFGFEENKIDRTFGIPEDFDYID 205

RESULT 4
ADM83810

ID ADM83810 standard; protein; 205 AA.

XX AC ADM83810;

XX DT 03-JUN-2004 (first entry)

XX DE Human cancer gene 121P1F1 protein #3.

XX KW Human; cancer gene 121P1F1, cytostatic; cancer; chromosome 4q; HLA;
XX KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
XX KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
XX KW cervical cancer; stomach cancer; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN US2003223997-A1.

XX PD 04-DEC-2003.

XX PF 28-FEB-2002; 2002US-00087190.

XX PK 08-FEB-2001; 2001US-00779250.

XX PA (CHAL//) CHAILITA-EID P M.

XX PA (HUBE//) HUBERT R S.

XX PA (RAIT//) RAITANO A B.

XX PA (FARI//) FARIS M.

XX PA (AFAR//) AFAR D E H.

XX PA (GEWV//) GE W.

XX PA (JAKO//) JAKOBOVITS A.

PI Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;

XX WPI; 2004-060522/06.

XX New composition comprising a substance that modulates the status of
XX 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
XX treating or preventing cancer e.g. prostate, bladder, colon, breast or
XX lung cancer.

XX Discloure; SEQ ID NO 20; 211pp; English.

XX The invention relates to a composition comprising a substance that
XX modulates the status of 121P1F1 (a protein encoded by a cancer expressed
XX gene) or a molecule that is modulated by 121P1F1 where status of the cell
XX that expresses 121P1F1 is modulated. Also included are a pharmaceutical
XX composition comprising the novel composition in a human unit dose form, a
XX recombinant protein comprising an antigen-binding region of a monoclonal
XX antibody, a non-human transgenic animal that produces an antibody, a
XX hybridoma that produces an antibody, a single chain monoclonal antibody
XX that immunospecifically binds to a 121P1F1-related protein (comprising
XX the variable domains of the heavy and light chains of a monoclonal
XX antibody), a vector comprising a polynucleotide that encodes a single
XX chain monoclonal antibody, a polynucleotide that encodes an analogue
XX peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
XX that expresses 121P1F1, inhibiting growth of cancer cells that expresses
XX 121P1F1 (comprising administering to the cells the composition), treating
XX a patient who bears cancer cells that express 121P1F1, generating a
XX mammalian immune response directed to 121P1F1, inducing an immune
XX response, monitoring 121P1F1 gene products in a biological sample from a
XX patient who has or who is suspected of having cancer, monitoring the
XX presence of cancer in an individual and an assay for detecting the
XX presence of a 121P1F1-related protein or polynucleotide in a biological
XX sample from a patient who has or who is suspected of having cancer. The
XX composition may comprise a polynucleotide that comprises a 121P1F1-
XX related protein coding sequence provided that the coding sequence does
XX not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
XX substance also comprises a polynucleotide that encodes at least one
XX peptide given in 16 Tables (given in the specification), the peptides
XX being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
XX splice variants. The composition is useful for detecting, treating or
XX preventing cancer, preferably prostate cancer, bladder cancer, kidney

CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC sequence is a 121P1F1 protein (full-length or fragment).
XX
SQ Sequence 205 AA;
Query Match 100.0%; Score 1047; DB 8; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKKGLSAEKKRTMMEIFSETKDVFOQLDKLEKIAPEKGTITANSVKYVLOSIVDDGAV 60
DB 1 MSKKKGLSAEKKRTMMEIFSETKDVFOQLDKLEKIAPEKGTITANSVKYVLOSIVDDGAV 60
QY 61 DCEKIGTSNYWAFPSKALHARKHKLVELESQSESGOKHSLQKSIIEKAKIGRCETER 120
DB 61 DCEKIGTSNYWAFPSKALHARKHKLVELESQSESGOKHSLQKSIIEKAKIGRCETER 120
QY 121 TRIAKELSSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAISMA 180
DB 121 TRIAKELSSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAISMA 180
QY 181 KRKGFEEKNKIDRTFGIPEDFDYID 205
DB 181 KRKGFEEKNKIDRTFGIPEDFDYID 205
RESULT 5
ADM83812 standard; protein; 205 AA.
ID ADM83812;
AC ADM83812;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human cancer gene 121P1F1 protein #5.
XX
KW Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
KW cervical cancer; stomach cancer; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN US00322397-A1.
XX
PD 04-DEC-2003.
XX
PF 28-FEB-2002; 2002US-00087190.
XX
PR 08-FEB-2001; 2001US-00779250.
XX
PA (CHAL/) CHALLITA-ETD P M.
PA (HUBE/) HUBERT R S.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (AFAR/) AFAR D E H.
PA (GEWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
XX Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;
XX
XX WPI; 2004-060522/06.
XX
XX
XX New composition comprising a substance that modulates the status of
PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.
XX
PS Disclosure; SEQ ID NO 22; 211pp; English.

XX
CC The invention relates to a composition comprising a substance that
CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
CC composition comprising the novel composition in a human unit dose form, a
CC recombinant protein comprising an antigen-binding region of a monoclonal
CC antibody, a non-human transgenic animal that produces an antibody, a
CC hybridoma that produces an antibody, a single chain monoclonal antibody
CC that immunospecifically binds to a 121P1F1-related protein (comprising
CC the variable domains of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
CC 121P1F1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121P1F1, generating a
CC mammalian immune response directed to 121P1F1, inducing an immune
CC response, monitoring 121P1F1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121P1F1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121P1F1-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides
CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC sequence is a 121P1F1 protein (full-length or fragment).
XX
SQ Sequence 205 AA;
Query Match 100.0%; Score 1047; DB 8; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKKGLSAEKKRTMMEIFSETKDVFOQLDKLEKIAPEKGTITANSVKYVLOSIVDDGAV 60
DB 1 MSKKKGLSAEKKRTMMEIFSETKDVFOQLDKLEKIAPEKGTITANSVKYVLOSIVDDGAV 60
QY 61 DCEKIGTSNYWAFPSKALHARKHKLVELESQSESGOKHSLQKSIIEKAKIGRCETER 120
DB 61 DCEKIGTSNYWAFPSKALHARKHKLVELESQSESGOKHSLQKSIIEKAKIGRCETER 120
QY 121 TRIAKELSSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAISMA 180
DB 121 TRIAKELSSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAISMA 180
QY 181 KRKGFEEKNKIDRTFGIPEDFDYID 205
DB 181 KRKGFEEKNKIDRTFGIPEDFDYID 205
RESULT 6
ADM83793 standard; protein; 205 AA.
ID ADM83793;
AC ADM83793;
XX
DT 03-JUN-2004 (first entry)
XX
XX
XX Human cancer gene 121P1F1 protein #1.
XX
XX Human cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;

KW cervical cancer; stomach cancer; gene therapy; vaccine.
 XX Homo sapiens.
 OS
 XX US2003223997-A1.
 PN
 XX 04-DEC-2003.
 PD
 XX 28-FEB-2002; 2002US-00087190.
 PF
 XX 08-FEB-2001; 2001US-00779250.
 PR
 XX (CHAL/) CHALLITA-EID P M.
 PA (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARIS M.
 PA (AFAR/) AFAR D E H.
 PA (GEWM/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
 PI Jakobovits A;
 DR WPI; 2004-060522/06.
 DR N-PSDB; ADM83792.
 XX
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121PI1 or a molecule that is modulated by 121PI1, useful for detecting,
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.
 PT
 PS Claim 19; SEQ ID NO 3; 211pp; English.
 XX
 XX The invention relates to a composition comprising a substance that
 CC modulates the status of 121PI1 (a protein encoded by a cancer expressed
 CC gene) or a molecule that is modulated by 121PI1 where status of the cell
 CC that expresses 121PI1 is modulated. Also included are a pharmaceutical
 CC composition comprising the novel composition in a human unit dose form, a
 CC recombinant protein comprising an antigen-binding region of a monoclonal
 CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody
 CC that immunospecifically binds to a 121PI1-related protein (comprising
 CC the variable domains of the heavy and light chains of a monoclonal
 CC antibody), a vector comprising a polynucleotide that encodes a single
 CC chain monoclonal antibody, a polynucleotide that encodes an analogue
 CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
 CC that expresses 121PI1, inhibiting growth of cancer cells that expresses
 CC 121PI1 (comprising administering to the cells the composition), treating
 CC a patient who bears cancer cells that express 121PI1, generating a
 CC mammalian immune response directed to 121PI1, inducing an immune
 CC response, monitoring 121PI1 gene products in a biological sample from a
 CC patient who has or who is suspected of having cancer, monitoring the
 CC presence of cancer in an individual and an assay for detecting the
 CC presence of a 121PI1-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC composition may comprise a polynucleotide that comprises a 121PI1-
 CC related protein coding sequence provided that the coding sequence does
 CC not encode the entire amino acid sequence of 121PI1 (ADM83793). The
 CC substance also comprises a polynucleotide that encodes at least one
 CC peptide given in 16 Tables (given in the specification), the peptides
 CC being HLA (human leukocyte antigen)-binding epitopes from 121PI1 or its
 CC splice variants. The composition is useful for detecting, treating or
 CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
 CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
 CC cervical cancer or stomach cancer. The composition can also be used as a
 CC vaccine to treat or prevent cancer that expresses or overexpresses
 CC 121PI1. The gene for 121PI1 is located on chromosome 4q. The present
 CC sequence is a 121PI1 protein (full-length or fragment).
 XX
 XX Sequence 205 AA;
 SQ
 Query Match 100.0%; Score 1047; DB 8; Length 205;
 Best local Similarity 100.0%; Pred. No. 1.5e-88;

Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSKKGLSAEKRRTMEIPESTKDVFLQKLEKIAPEKKGITANSVKEVQLSLVDDGV 60
 DB 1 MSKKGLSAEKRRTMEIPESTKDVFLQKLEKIAPEKKGITANSVKEVQLSLVDDGV 60
 QY 61 DCEIRIGTSNYWAFPSKALHARKHKLVELESQLSBGSQKHASLQKSIKAKIGRCETSR 120
 DB 61 DCEIRIGTSNYWAFPSKALHARKHKLVELESQLSBGSQKHASLQKSIKAKIGRCETSR 120
 QY 121 TRLAKEISSLDRQRLAEVEKYKDCDPQVEEIRQANKYAKKAAWNTNIPAIKSWA 180
 DB 121 TRLAKEISSLDRQRLAEVEKYKDCDPQVEEIRQANKYAKKAAWNTNIPAIKSWA 180
 QY 181 KRKGFSEENKIDRTGPIPEDFDYID 205
 DB 181 KRKGFSEENKIDRTGPIPEDFDYID 205
 RESULT 7
 ID ADM83811 standard; protein; 205 AA.
 XX
 XX ADM83811;
 AC
 XX
 XX 03-JUN-2004 (first entry)
 DT
 XX
 XX Human cancer gene 121PI1 protein #4.
 DE
 XX
 XX Human; cancer gene 121PI1; cytostatic; cancer; chromosome 4q; HLA;
 KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
 KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KW cervical cancer; stomach cancer; gene therapy; vaccine.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2003223997-A1.
 PN
 XX 04-DEC-2003.
 PD
 XX 28-FEB-2002; 2002US-00087190.
 PF
 XX 08-FEB-2001; 2001US-00779250.
 PR
 XX (CHAL/) CHALLITA-EID P M.
 PA (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARIS M.
 PA (AFAR/) AFAR D E H.
 PA (GEWM/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
 PI Jakobovits A;
 DR WPI; 2004-060522/06.
 DR N-PSDB; ADM83792.
 XX
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121PI1 or a molecule that is modulated by 121PI1, useful for detecting,
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.
 PT
 PS Disclosure; SEQ ID NO 21; 211pp; English.
 XX
 XX The invention relates to a composition comprising a substance that
 CC modulates the status of 121PI1 (a protein encoded by a cancer expressed
 CC gene) or a molecule that is modulated by 121PI1 where status of the cell
 CC that expresses 121PI1 is modulated. Also included are a pharmaceutical
 CC composition comprising the novel composition in a human unit dose form, a
 CC recombinant protein comprising an antigen-binding region of a monoclonal
 CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody
 CC that immunospecifically binds to a 121PI1-related protein (comprising

CC the variable domains of the heavy and light chains of a monoclonal
 CC antibody), a vector comprising a polynucleotide that encodes a single
 CC chain monoclonal antibody, a polynucleotide that encodes an analogue
 CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
 CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
 CC 121P1F1 (comprising administering to the cells the composition), treating
 CC a patient who bears cancer cells that express 121P1F1, generating a
 CC mammalian immune response directed to 121P1F1, inducing an immune
 CC response, monitoring 121P1F1 gene products in a biological sample from a
 CC patient who has or who is suspected of having cancer, monitoring the
 CC presence of cancer in an individual and an assay for detecting the
 CC presence of a 121P1F1-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC composition may comprise a polynucleotide that comprises a 121P1F1-
 CC related protein coding sequence provided that the coding sequence does
 CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
 CC substance also comprises a polynucleotide that encodes at least one
 CC peptide given in 16 Tables (given in the specification), the peptides
 CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
 CC splice variants. The composition is useful for detecting, treating or
 CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
 CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
 CC cervical cancer or stomach cancer. The composition can also be used as a
 CC vaccine to treat or prevent cancer that expresses or overexpresses
 CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
 CC sequence is a 121P1F1 protein (full-length or fragment).

XX SQ Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 8; Length 205;

Best Local Similarity 100.0%; Pred. No. 1.5e-88; Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEKKRTMMEIFSETKQVFOQLDKLEKIAPEKGTITAMSVKYLQSLVDDGNV 60
 Db 1 MSKKKGLSAEKKRTMMEIFSETKQVFOQLDKLEKIAPEKGTITAMSVKYLQSLVDDGNV 60
 QY 61 DCRIGTSNYWYAFPSKALHARKHKLVELESQSLSEGSQKHAISLOKSTIEKAKIGRCETERR 120
 Db 61 DCRIGTSNYWYAFPSKALHARKHKLVELESQSLSEGSQKHAISLOKSTIEKAKIGRCETERR 120
 QY 121 TRLAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIFAIKSWA 180
 Db 121 TRLAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIFAIKSWA 180
 QY 181 KRRFGFENKIDRTFGIPEDFDYID 205
 Db 181 KRRFGFENKIDRTFGIPEDFDYID 205

RESULT 8

ID ADM83804 standard; protein; 205 AA.

XX ADM83804;

XX DT 03-JUN-2004 (first entry)

XX DB Human cancer gene 121P1F1 protein #2.

KW Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
 KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
 KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KW cervical cancer; stomach cancer; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN US2003223997-A1.

XX PD 04-DEC-2003.

XX PF 28-FEB-2002; 2002US-00087190.

PR 08-FEB-2001; 2001US-00779250.

XX (CHAL/) CHALLITA-EID P. M.
 XX (HUBE/) HUBERT R. S.
 XX (RAIT/) RAITANO A. B.
 XX (FARI/) FARIS M.
 XX (AFAR/) AFAR D. E. H.
 XX (GEWM/) GE W.
 XX (JAKO/) JAKOBOVITS A.

PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
 XX Jakobovits A;
 XX WPI; 2004-060522/06.

PT New composition comprising a substance that modulates the status of
 PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.

XX Disclosure; SEQ ID NO 14; 211pp; English.

CC The invention relates to a composition comprising a substance that
 CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
 CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
 CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
 CC composition comprising the novel composition in a human unit dose form, a
 CC recombinant protein comprising an antigen-binding region of a monoclonal
 CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody
 CC that immunospecifically binds to a 121P1F1-related protein (comprising
 CC the variable domains of the heavy and light chains of a monoclonal
 CC antibody), a vector comprising a polynucleotide that encodes a single
 CC chain monoclonal antibody, a polynucleotide that encodes an analogue
 CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
 CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
 CC 121P1F1 (comprising administering to the cells the composition), treating
 CC a patient who bears cancer cells that express 121P1F1, generating a
 CC mammalian immune response directed to 121P1F1, inducing an immune
 CC response, monitoring 121P1F1 gene products in a biological sample from a
 CC patient who has or who is suspected of having cancer, monitoring the
 CC presence of cancer in an individual and an assay for detecting the
 CC presence of a 121P1F1-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC composition may comprise a polynucleotide that comprises a 121P1F1-
 CC related protein coding sequence provided that the coding sequence does
 CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
 CC substance also comprises a polynucleotide that encodes at least one
 CC peptide given in 16 Tables (given in the specification), the peptides
 CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
 CC splice variants. The composition is useful for detecting, treating or
 CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
 CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
 CC cervical cancer or stomach cancer. The composition can also be used as a
 CC vaccine to treat or prevent cancer that expresses or overexpresses
 CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
 CC sequence is a 121P1F1 protein (full-length or fragment).

XX SQ Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 8; Length 205;

Best Local Similarity 100.0%; Pred. No. 1.5e-88; Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEKKRTMMEIFSETKQVFOQLDKLEKIAPEKGTITAMSVKYLQSLVDDGNV 60
 Db 1 MSKKKGLSAEKKRTMMEIFSETKQVFOQLDKLEKIAPEKGTITAMSVKYLQSLVDDGNV 60
 QY 61 DCRIGTSNYWYAFPSKALHARKHKLVELESQSLSEGSQKHAISLOKSTIEKAKIGRCETERR 120
 Db 61 DCRIGTSNYWYAFPSKALHARKHKLVELESQSLSEGSQKHAISLOKSTIEKAKIGRCETERR 120
 QY 121 TRLAKELSLRDQREOLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIFAIKSWA 180

Db 121 TRLAKELSLDQREQLKAEVEKXKDCDPQVEEIRQANKVAKKAEANRWNTDNIFAIKSWA 180
 QY 181 KRKGFEEENKIDRTFGIPEDFDYID 205
 Db 181 KRKGFEEENKIDRTFGIPEDFDYID 205

RESULT 9

ABP75541
 ID ABP75541 standard; protein, 219 AA.

XX AC ABP75541;
 XX DT 10-FEB-2003 (first entry)

XX DE Human secretory polypeptide SPTM SEQ ID NO 725.

KM Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
 KM asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
 KM Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
 KM multiple sclerosis; Parkinson's disease; cell proliferative disorder;
 KM anti-inflammatory; immunosuppressive; neuroprotective; nootropic;
 KM neuroleptic; anticonvulsant; cyostatic; antiparkinsonian; anxiolytic;
 KM antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;
 KM secretory polynucleotide; secretory protein.

OS Homo sapiens.

XX PN WO200283876-A2.

XX PD 24-OCT-2002.

XX PF 27-MAR-2002; 2002WO-US009921.

XX PR 29-MAR-2001; 2001US-0280067P.

XX PR 29-MAR-2001; 2001US-0280068P.

XX PR 16-MAY-2001; 2001US-0291280P.

XX PR 17-MAY-2001; 2001US-0291829P.

XX PR 17-MAY-2001; 2001US-0291849P.

XX PR 19-JUN-2001; 2001US-0299428P.

XX PR 20-JUN-2001; 2001US-0299776P.

XX PR 20-JUN-2001; 2001US-0300001P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshy SR;
 PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Matwaha R, Lo A, Ian RY, Urashka ME;
 XX DR MPI; 2003-075543/07.
 XX DR N-PSDB; AB235987.

XX PT New human secretory proteins and polynucleotides, useful for diagnosing,
 PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
 PT neurological disorders (e.g. Alzheimer's), or cell proliferations or
 PT cancers.

XX PS Claim 27; SEQ ID NO 725; 458bp + Sequence Listing; English.

XX CC The invention relates to a secretory polynucleotide (designated sptm)
 CC comprising any of 567 polynucleotide sequences (AB235837-AB236403), a
 CC naturally occurring polynucleotide sequence at least 90 % identical to
 CC the polynucleotide sequence, a polynucleotide complementary to them or an
 CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
 CC treating, preventing or diagnosing a disease or condition associated with
 CC the expression of functional SPTM. These are particularly useful for
 CC diagnosing, treating or preventing autoimmune/inflammatory disorders
 CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
 CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
 CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,

CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
 CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
 CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
 CC breast, cervix or prostate). The present sequence is one of the SPTM
 CC proteins of the invention (ABP75384-ABP75962). Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 219 AA;

Query Match 100.0%; Score 1047; DB 6; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1,7e-88;
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSLAEKRRRMETFEETQVQKLEKIAPEKKTMTMSYKVEQSLVDQMV 60
 Db 15 MSKKKGSLAEKRRRMETFEETQVQKLEKIAPEKKTMTMSYKVEQSLVDQMV 74
 QY 61 DCEKIGTSNYWAPPSPKALHARKKLEYLEESQSEGSQKASLQKIEKAKIGRCETEE 120
 Db 75 DCEKIGTSNYWAPPSPKALHARKKLEYLEESQSEGSQKASLQKIEKAKIGRCETEE 134
 QY 121 TRLAKELSLDQREQLKAEVEKXKDCDPQVEEIRQANKVAKKAEANRWNTDNIFAIKSWA 180
 Db 135 TRLAKELSLDQREQLKAEVEKXKDCDPQVEEIRQANKVAKKAEANRWNTDNIFAIKSWA 194
 QY 181 KRKGFEEENKIDRTFGIPEDFDYID 205
 Db 195 KRKGFEEENKIDRTFGIPEDFDYID 219

RESULT 10

ADM83834
 ID ADM83834 standard; protein, 206 AA.

XX AC ADM83834;

XX DT 03-JUN-2004 (first entry)

XX DE Human cancer gene 121P1F1 variant protein #1.

XX KW Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
 KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
 KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KW cervical cancer; stomach cancer; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN US2003223997-A1.

XX PD 04-DEC-2003.

XX PF 28-FEB-2002; 2002US-00087190.

XX PR 08-FEB-2001; 2001US-00779250.

XX PA (CHAL/) CHALLITA-EID P M.

XX PA (HUBE/) HUBERT R S.

XX PA (RAIT/) RAITANO A B.

XX PA (FARI/) FARIS M.

XX PA (AFAR/) AFAR D E H.

XX PA (GEW/) GE W.

XX PI (JAKO/) JAKOBOVITS A.

XX PI Chalita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
 XX PI Jakobovits A;

XX DR MPI; 2004-060522/06.

XX PT New composition comprising a substance that modulates the status of
 PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,

PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.

PS Example 5; SEQ ID NO 44; 211pp; English.

The invention relates to a composition comprising a substance that modulates the status of 121P1P1 (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121P1P1 where status of the cell that expresses 121P1P1 is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a hybridoma that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121P1P1-related protein (comprising the variable domains of the heavy and light chains of a monoclonal antibody), a vector comprising a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes an analogue peptide, delivering a cytotoxic agent or a diagnostic agent to a cell that expresses 121P1P1, inhibiting growth of cancer cells that expresses 121P1P1 (comprising administering to the cells the composition), treating a patient who bears cancer cells that express 121P1P1, generating a mammalian immune response directed to 121P1P1, inducing an immune response, monitoring 121P1P1 gene products in a biological sample from a patient who has or who is suspected of having cancer, monitoring the presence of cancer in an individual and an assay for detecting the presence of a 121P1P1-related protein or polynucleotide in a biological sample from a patient who has or who is suspected of having cancer. The composition may comprise a polynucleotide that comprises a 121P1P1-related protein coding sequence provided that the coding sequence does not encode the entire amino acid sequence of 121P1P1 (ADM83793). The substance also comprises a polynucleotide that encodes at least one peptide given in 16 tables (given in the specification), the peptides being HLA (human leukocyte antigen)-binding epitopes from 121P1P1 or its splice variants. The composition is useful for detecting, treating or preventing cancer, preferably prostate cancer, bladder cancer, kidney cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer, cervical cancer or stomach cancer. The composition can also be used as a vaccine to treat or prevent cancer that expresses or overexpresses 121P1P1. The gene for 121P1P1 is located on chromosome 4q. The present sequence is a 121P1P1 protein (full-length or fragment).

SQ Sequence 206 AA:

Query Match	99.0%;	Score 1036.5;	DB 8;	Length 206;
Best Local Similarly	99.5%;	Pred. No. 1.4e-87;		
Matches 205; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1;

Qy	1	MSKKKGISAEKKTMMEEIFSETKOVFOJKDEKTAPEKKGITMMSVEVQLSLVDGMV	60
Db	1	MSKKKGISAEKKTMMEEIFSETKOVFOJKDEKTAPEKKGITMMSVEVQLSLVDGMV	60
Qy	61	DCERIGTSNYMYAPSKALHARKHKLVELES-QISEGSGQKASLOKSIIEKAKICRTEE	119
Db	61	DCERIGTSNYMYAPSKALHARKHKLVELESQQLSESGQKASIQKSIIEKAKICRTEE	120
Qy	120	RTLALAEISLRDREQLAEVEKTKCDPQVVEEIRIQRANKYAEANRMTDNI PAIKSW	179
Db	121	RTLALAEISLRDREQLAEVEKTKCDPQVVEEIRIQRANKYAEANRMTDNI PAIKSW	180
Qy	180	AKRKFGFEENKIDRTGIPEDPDYID 205	
Db	181	AKRKFGFEENKIDRTGIPEDPDYID 206	

RESULT 11

ID ADM83835 standard; protein; 206 AA.

AC ADM838357

DT 03-JUN-2004 (first entry)

DE Human cancer gene 121P1F1 variant protein #2.

XX Human: cancer gene 121P1P1; cytostatic; cancer; chromosome 4q; HLA;
 KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer
 KM colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KM cervical cancer; stomach cancer; gene therapy; vaccine.

OS Homo sapiens.

PN US2003223997-A1.

PD 04-DEC-2003.

PF 28-FEB-2002; 2002US-00087190.

PR 08-FEB-2001; 2001US-00779250.

PA (CHAL/) CHALLITA-EID P M.

PA (RAIT/) RAITANO A B.

PA (AFAR/) AFAR D E H.

PA (JAKO/) JAKBOVITS

PI Chailita-Eid PM, H

XX

XX

PT 121PIF1 or a molecule that is modulated by 121PIF1, useful for detecting

PT lung cancer.

PS Example 5; SEQ ID NO 45; 211pp; English.

The invention relates to a composition comprising a substance that modulates the status of 121P1F1 (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121P1F1 where status of the cell that expresses 121P1F1 is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a hybridoma that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121P1F1-related protein (comprising the variable domains of the heavy and light chains of a monoclonal antibody), a vector comprising a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes an analogue peptide, delivering a cytotoxic agent or a diagnostic agent to a cell that expresses 121P1F1, inhibiting growth of cancer cells that expresses 121P1F1 (comprising administering to the cells the composition), treating a patient who bears cancer cells that express 121P1F1, generating a mammalian immune response directed to 121P1F1, inducing an immune response, monitoring 121P1F1 gene products in a biological sample from a patient who has or who is suspected of having cancer, monitoring the presence of cancer in an individual and an assay for detecting the presence of a 121P1F1-related protein or polynucleotide in a biological sample from a patient who has or who is suspected of having cancer. The composition may comprise a polynucleotide that comprises a 121P1F1-related protein coding sequence provided that the coding sequence does not encode the entire amino acid sequence of 121P1F1 (ADM83793). The substance also comprises a polynucleotide that encodes at least one peptide given in 16 Tables (given in the specification), the peptides being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its splice variants. The composition is useful for detecting, treating or preventing cancer, preferably prostate cancer, bladder cancer, kidney cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer, cervical cancer or stomach cancer. The composition can also be used as a vaccine to treat or prevent cancer that expresses or overexpresses 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present sequence is a 121P1F1 protein (full-length or fragment).

Sequence 206 AA;

Query Match 99.0%; Score 1036.5; DB 8; Length 206;
 Best Local Similarity 99.5%; Pred. No. 1.4e-87;
 Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSKKGLSAEKKRTMMEIFSETKQVFOLEKIAPKKGTITANSVKEVLSLVDDGAV 60
 DB 1 MSKKGLSAEKKRTMMEIFSETKQVFOLEKIAPKKGTITANSVKEVLSLVDDGAV 60
 QY 61 DERIGTSNYWAFPSKALHARKHKLVEVLSQSGSHASLQKSIKAKIGRCETEE 119
 DB 61 DERIGTSNYWAFPSKALHARKHKLVEVLSQSGSHASLQKSIKAKIGRCETEE 120
 QY 120 RTRLAKELSLRDQREOLKAEVEKYKDCDPQVEEIRQANKYAKKXANRMTDNIPAIKSM 179
 DB 121 RTRLAKELSLRDQREOLKAEVEKYKDCDPQVEEIRQANKYAKKXANRMTDNIPAIKSM 180
 QY 180 AKRKGFEENKIDRTFGIPEDFDYID 205
 DB 181 AKRKGFEENKIDRTFGIPEDFDYID 206

RESULT 12
 ADM83814 standard; protein; 198 AA.
 XX ID ADM83814;
 XX AC ADM83814;
 XX DT 03-JUN-2004 (first entry)
 XX DE Human cancer gene 121P1F1 protein fragment.
 XX KM Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
 KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
 KM colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KM cervical cancer; stomach cancer; gene therapy; vaccine.
 XX OS Homo sapiens.
 XX PN US2003223997-A1.
 XX PD 04-DEC-2003.
 XX PF 28-FEB-2002; 2002US-00087190.
 XX PR 08-FEB-2001; 2001US-00779250.
 XX PA (CHAL/) CHALLITA-EID P M.
 PA (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) PARIS M.
 PA (AFAR/) AFAR D E H.
 PA (GEWU/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX PI Challaite-Bid PM, Hubert RS, Raitano AB, Paris M, Afar DEH, Ge W;
 PI Jakobovits A;
 XX DR WPI; 2004-060522/06.
 XX PT New composition comprising a substance that modulates the status of
 PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.
 XX Example 2; SEQ ID NO 24; 211pp; English.
 CC The invention relates to a composition comprising a substance that
 CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
 CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
 CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
 CC composition comprising the novel composition in a human unit dose form, a
 CC recombinant protein comprising an antigen-binding region of a monoclonal

CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody
 CC that immunospecifically binds to a 121P1F1-related protein (comprising
 CC the variable domains of the heavy and light chains of a monoclonal
 CC antibody), a vector comprising a polynucleotide that encodes a single
 CC chain monoclonal antibody, a polynucleotide that encodes an analogue
 CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
 CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
 CC 121P1F1 (comprising administering to the cells the composition), treating
 CC a patient who bears cancer cells that express 121P1F1, generating a
 CC mammalian immune response directed to 121P1F1, inducing an immune
 CC response, monitoring 121P1F1 gene products in a biological sample from a
 CC patient who has or who is suspected of having cancer, monitoring the
 CC presence of cancer in an individual and an assay for detecting the
 CC presence of a 121P1F1-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC composition may comprise a polynucleotide that comprises a 121P1F1-
 CC related protein coding sequence provided that the coding sequence does
 CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
 CC substance also comprises a polynucleotide that encodes at least one
 CC peptide given in 16 Tables (given in the specification), the peptides
 CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
 CC splice variants. The composition is useful for detecting, treating or
 CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
 CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
 CC cervical cancer or stomach cancer. The composition can also be used as a
 CC vaccine to treat or prevent cancer that expresses or overexpresses
 CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
 CC sequence is a 121P1F1 protein (full-length or fragment).
 XX SQ Sequence 198 AA;

Query Match 96.6%; Score 1011; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 3.1e-85;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KGLSAEKKRTMMEIFSETKQVFOLEKIAPKKGTITANSVKEVLSLVDDGAVDCER 64
 DB 1 KGLSAEKKRTMMEIFSETKQVFOLEKIAPKKGTITANSVKEVLSLVDDGAVDCER 60
 QY 65 IGTSNYWAFPSKALHARKHKLVEVLSQSGSHASLQKSIKAKIGRCETERTRLA 124
 DB 61 IGTSNYWAFPSKALHARKHKLVEVLSQSGSHASLQKSIKAKIGRCETERTRLA 120
 QY 125 KELSLRQREOLKAEVEKYKDCDPQVEEIRQANKYAKKXANRMTDNIPAIKSAKRF 184
 DB 121 KELSLRQREOLKAEVEKYKDCDPQVEEIRQANKYAKKXANRMTDNIPAIKSAKRF 180
 QY 185 GFEENKIDRTFGIPEDFD 202
 DB 181 GFEENKIDRTFGIPEDFD 198

RESULT 13
 AAM40043 standard; protein; 190 AA.
 XX ID AAM40043;
 XX AC AAM40043;
 XX DT 22-OCT-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 3188.
 XX KM Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KM peripheral nervous system; neuropathy; central nervous system; CNS;
 KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KM chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KM leukaemia.
 XX OS Homo sapiens.
 XX PN WO200153312-A1.

XX 26-JUL-2001.
PD
XX
PF 26-DEC-2000; 2000MO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QH,
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI59199.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Example 4; SEQ ID NO 3188; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAI38642-AAI42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, and
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 190 AA;
XX
Query Match 93.1%; Score 975; DB 4; Length 190;
Best Local Similarity 100.0%; Pred. No. 6.3e-82;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 16 MMEIFSETKDVPOLKDLKIAPEKEGITTAMSVKEVLSQSLVDGMDVCERIGTSNYWAPF 75
DB 1 MMEIFSETKDVPOLKDLKIAPEKEGITTAMSVKEVLSQSLVDGMDVCERIGTSNYWAPF 60
XX
QY 76 SKALHARKHKLLEVLSESGSQKIASLQKSIKAKIGRCETEERTRLAKELSSLRDQRE 135
DB 61 SKALHARKHKLLEVLSESGSQKIASLQKSIKAKIGRCETEERTRLAKELSSLRDQRE 120
XX
QY 136 QLKAEVEKYKDDCPPOVEEIRQANKVAKAANRWTDNIFAIKSWAKRKGFEENKIDRTF 195
DB 121 QLKAEVEKYKDDCPPOVEEIRQANKVAKAANRWTDNIFAIKSWAKRKGFEENKIDRTF 180
XX
QY 196 GIPEDFDYID 205
DB 181 GIPEDFDYID 190
XX
RESULT 14
ADD84547
ID ADD84547 standard; protein; 190 AA.
XX
AC ADD84547;

XX 29-JAN-2004 (first entry)
DT
XX
DE 121PI1 variant 4 protein.
XX
XX 121PI1, 121PI1 modulation; human; chromosome 4q; cytostatic;
KM gene therapy; vaccine; cancer; immune response; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200295009-A2.
XX
PD 28-NOV-2002.
XX
XX 28-FEB-2002; 2002MO-US006242.
XX
PR 05-MAR-2001; 2001US-00799250.
XX (AGEN-) AGENSYS INC.
XX
PI Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
PI Jakobovits A;
XX
DR WPI; 2003-156757/15.
DR N-PSDB; ADD84546.
XX
PT Composition comprising a substance that modulates the status of 121PI1,
XX useful in diagnosing, preventing, prognosticating or treating patients
XX with cancer that expresses 121PI1, such as breast, colon, ovarian or
XX lung cancer.
XX
PS Claim 19; Fig 2F; 285pp; English.
XX
CC The present invention describes a composition (I) comprising a substance
CC that modulates the status of 121PI1 (gene and encoded protein), or a
CC molecule that is modulated by 121PI1, where the status of a cell that
CC expresses 121PI1 is modulated. The human 121PI1 gene maps to chromosome
CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
CC vaccines. The composition (I) can be used for diagnosing, preventing,
CC prognosticating or treating patients with cancer that expresses 121PI1,
CC such as breast, colon, ovarian or lung cancer. The 121PI1 gene or its
CC fragment can be used to elicit a humoral or cellular immune response.
CC 121PI1 antibodies can be used in active or passive immunisation. 121PI1
CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121PI1 genes, as coding sequences for directing the
CC expression of 121PI1 polypeptides, or as tools for modulating or
CC inhibiting the expression of 121PI1 genes. The present sequence is used
CC in the exemplification of the present invention.
XX
SQ Sequence 190 AA;
XX
Query Match 93.1%; Score 975; DB 7; Length 190;
Best Local Similarity 100.0%; Pred. No. 6.3e-82;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 16 MMEIFSETKDVPOLKDLKIAPEKEGITTAMSVKEVLSQSLVDGMDVCERIGTSNYWAPF 75
DB 1 MMEIFSETKDVPOLKDLKIAPEKEGITTAMSVKEVLSQSLVDGMDVCERIGTSNYWAPF 60
XX
QY 76 SKALHARKHKLLEVLSESGSQKIASLQKSIKAKIGRCETEERTRLAKELSSLRDQRE 135
DB 61 SKALHARKHKLLEVLSESGSQKIASLQKSIKAKIGRCETEERTRLAKELSSLRDQRE 120
XX
QY 136 QLKAEVEKYKDDCPPOVEEIRQANKVAKAANRWTDNIFAIKSWAKRKGFEENKIDRTF 195
DB 121 QLKAEVEKYKDDCPPOVEEIRQANKVAKAANRWTDNIFAIKSWAKRKGFEENKIDRTF 180
XX
QY 196 GIPEDFDYID 205
DB 181 GIPEDFDYID 190

RESULT 15
ADM83857
ID ADM83857 standard; protein; 190 AA.
XX
AC ADM83857;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human cancer gene 121P1F1 protein 16-205.
XX
KM Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
KM cervical cancer; stomach cancer; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN US2003223997-A1.
XX
PD 04-DEC-2003.
XX
PF 28-FEB-2002; 2002US-00087190.
XX
PR 08-FEB-2001; 2001US-00779250.
XX
PA (CHAL/) CHALLITA-EID P M.
PA (HUBE/) HUBERT R S.
PA (RAT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (AFAR/) AFAR D E H.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;
XX
DR WPI; 2004-060522/06.
XX
PT New composition comprising a substance that modulates the status of
PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.
XX
PS Example 5; SEQ ID NO 67; 211pp; English.
XX
CC The invention relates to a composition comprising a substance that
CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
CC composition comprising the novel composition in a human unit dose form, a
CC recombinant protein comprising an antigen-binding region of a monoclonal
CC antibody, a non-human transgenic animal that produces an antibody, a
CC hybridoma that produces an antibody, a single chain monoclonal antibody
CC that immunospecifically binds to a 121P1F1-related protein (comprising
CC the variable domains of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
CC 121P1F1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121P1F1, generating a
CC mammalian immune response directed to 121P1F1, inducing an immune
CC response, monitoring 121P1F1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121P1F1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121P1F1-
CC related protein coding sequence, provided that the coding sequence does
CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides
CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its

CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC sequence is a 121P1F1 protein (full-length or fragment).
XX
SQ Sequence 190 AA;
XX
Query Match 93.1%; Score 975; DB 8; Length 190;
Best Local Similarity 100.0%; Pred. No. 6.3e-82;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 16 MMEIFSRKDVYFQLDLEKIAPEKEGITAMSVKEVLAQSLVDGWDCCRIGTSNYMAFP 75
Db 1 MMEIFSRKDVYFQLDLEKIAPEKEGITAMSVKEVLAQSLVDGWDCCRIGTSNYMAFP 60
XX
QY 76 SKALHARKHKLVELESQSLSEGSQKHAQLQKSIKAKIGRCETERTRLAKELSLRDQRE 135
Db 61 SKALHARKHKLVELESQSLSEGSQKHAQLQKSIKAKIGRCETERTRLAKELSLRDQRE 120
XX
QY 136 QKAEVEKXKCDPQVVEBIRQANKVAKAANRWTDNIFAIKSNKRGFEENKIDRTF 195
Db 121 QKAEVEKXKCDPQVVEBIRQANKVAKAANRWTDNIFAIKSNKRGFEENKIDRTF 180
XX
QY 196 GIPEDFDYID 205
Db 181 GIPEDFDYID 190

Search completed: July 27, 2005, 09:37:57
Job time : 166 secs

This Page Blank (uspto)

~~UNAVAILABLE COPY~~

A;Molecule type:

M. / MOU, H. / MOLLER, A.S. / COLUCCI, D.S. / CHEN, H. / VALENZUELA, C.E. / SINGH, S. /

M. / MOU, H. / MOLLER, A.S. / COLUCCI, D.S. / CHEN, H. / VALENZUELA, C.E. / SINGH, S. /

submitted to the Protein Sequence Database, April 1996

A:Reference number: S62997

A:Accession: S63011

A:Molecule type: DNA

A:Residues: 1-199 <POW>

A:Cross-references: EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL07

A:Experimental source: strain S288C

R:Solier-Mira, A.; Saliz, J.E.; Ballesta, J.P.G.; Remacha, M.

A:Submitted to the Protein Sequence Database, April 1996

A:Reference number: S63018

A:Accession: S63018

A:Molecule type: DNA

A:Residues: 1-199 <SOL>

A:Cross-references: EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL07

A:Experimental source: strain S288C

R:Poehlmann, R.; Philippson, P.

Yeast 12, 391-402, 1996

A:Title: Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 12

A:Reference number: S63925; PMID:8701611

A:Accession: S63928

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-199 <POF>

A:Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

C:Genetics:

A:Gene: SGD:TPM1

A:Cross-references: SGD:S0005023; MIPS:YNL079C

A:Map position: 14L

C:Superfamily: tropomyosin TPM1

C:Keywords: coiled coil; cytoskeleton

Query Match 10.8%; Score 113; DB 2; Length 199;

Best Local Similarity 24.7%; Pred. No. 1;

Matches 46; Conservative 40; Mismatches 54; Indels 46; Gaps 8;

7 TSAEERKRTMMEIFSETKQVFOVKDLEKTAPEKKGITAMSVKVLQSLVDD-----GMV 60

13 LRAESQKEKEKEKKEKKEKLEQ-ENVE---KENQKSLTVKN--QQLDEIKLEAGIS 65

61 DCEIRIGTSNYWAFPSKALHARKHKL-----EVLSEQLSESG-----SOK 99

66 DSKQTEQDNVKEKNQKSLTVKNHQLSEELKEALSLASKQLSEDSHHLQSNNDNFSKX 125

100 HASLQKISIKAKIGRCETEERTR-----LAKELSSLRDQEQKAAVE---KYKCC 147

126 NQQLDEEDLESPTKLEETTEKLRSDLKADQLERRVVALEQREWERKNEELTVYEDA 185

148 DPQVVE 153

186 KKELEDR 191

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Query Match 10.7%; Score 112; DB 2; Length 284;

Best Local Similarity 22.7%; Pred. No. 1.8;

Matches 48; Conservative 41; Mismatches 74; Indels 48; Gaps 9;

1 MSKKKGLSAEE---KRTMMEIFSETKQVFO-----LKDLKTAPEK-EKGITAMSV 47

73 LARKKATDAEADVASLNRRIQLVEEELDRADQERLATALQKLEAEKADSESGMKVLEN 132

48 KEVLQSLVDGKVDCEIRIGTSNYWAFPSKALHARKHKLTVLESQLSESGSK---HSL 103

133 R---ALDDEKEMELQEI-----QLQEKHIAEADRKREYEVARKLVIIEGDL 176

104 OKSIEKATL--GRCEETEERTLAKELSLRDQEQKAAVEKYKCDPQVVEIRQANKV 161

177 ERAERKALSEKGC-----ALEEELKTVTNKLSLEQAARKYSQKEKREYEIKVLTDK 231

162 AKKANRWTDNIFAIKSWAKRKFGEENKID 192

232 LKEAETR-----AEFAERTVAKLEKSID 254

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 09:23:03 ; Search time 174 Seconds
(without alignments)

603.312 Million cell updates/sec

Title: US-10-087-190-3
Perfect score: 1047
Sequence: 1 MSKKKGLSAEKRTIMEIF.....FEENKIDRTFGIPEDFDYID 205

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047	100.0	205	2	Q9BWT6
2	954	91.1	205	2	Q8K396
3	948	90.5	205	2	Q9DDA1
4	644	61.5	220	2	Q6DC61
5	462	44.1	196	2	Q86E28
6	440	42.0	230	2	Q8GYD2
7	427	40.8	207	2	Q6H432
8	349	33.3	210	1	YAS3 SCHPO
9	340.5	32.5	203	2	Q8SUA9
10	340.5	32.5	203	2	Q6WDA3
11	340.5	32.5	203	2	Q7GT0X
12	332.5	31.8	179	2	Q6Q9F9
13	277	26.5	196	2	Q7RH53
14	266.5	25.5	215	2	Q6B0L5
15	221	21.1	225	2	Q7SC55
16	206.5	19.7	225	2	Q6CSX5
17	197	18.8	128	2	Q9S2E5
18	175	16.7	222	2	Q6FL56
19	168.5	16.1	174	1	YGT3 YEAST
20	153.5	14.7	101	2	Q6B679
21	136.5	13.0	1281	2	Q7T2F8
22	135.5	12.9	910	2	DYNA MOUSE
23	134.5	12.8	890	2	Q6AMB1
24	134.5	12.8	890	2	Q6AMB3
25	134.5	12.8	1139	2	Q6I037
26	134.5	12.8	1264	2	Q6NZM3
27	134.5	12.8	1278	1	DYNA_HUMAN
28	134.5	12.8	1278	2	Q6MZ23
29	131.5	12.6	1280	1	DYNA RAT
30	130.5	12.5	1224	1	DYNA_CHICK
31	126.5	12.1	1232	2	Q6PCJ1

32	126	12.0	609	2	Q8TXA4
33	122.5	11.7	797	2	Q6GLB3
34	122	11.7	10578	2	Q8ISF5
35	122	11.7	18519	2	Q8ISF6
36	122	11.7	18534	2	Q8ISF7
37	121.5	11.6	995	2	Q6FIN4
38	121.5	11.6	1357	1	KTNI_HUMAN
39	121.5	11.6	1364	1	KTNI_CHICK
40	120.5	11.5	172	2	Q82AV3
41	120.5	11.5	448	2	Q84H59
42	120.5	11.5	1732	2	Q9VJ35
43	120	11.5	882	1	RAS0_PYRPU
44	120	11.5	1120	1	ERCI_MOUSE
45	118.5	11.3	1177	2	Q877I1

ALIGNMENTS

RESULT 1					
ID	Q9BWT6	PRELIMINARY:	PRT:	205 AA.	
AC	Q9BWT6				
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DT	25-OCT-2004	(TREMBLrel. 26, Last annotation update)			
DE	GAL				
CN	Name=GAL;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Solis G., Hoter H.W.;				
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISUE=Lymph;				
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bock N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hogg L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshitoki S., Carrinci R., Prange C.,				
RA	Rahk S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,				
RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smalhe U., Smalhe D.E., Scherch A., Schin J.E.,				
RA	Jones S.J., Maitra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RP	[3]				
RC	SEQUENCE FROM N.A.				
RC	TISUE=Lymph;				
RA	Strausberg R.;				
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY028916; AAK26168.1; -				
DR	EMBL; BC032142; AAH32142.1; -				
DR	InterPro; IPR005647; Mnd1.				
DR	InterPro; IPR009058; wing_hlx_DNA_bnd.				
DR	Pfam; PF03962; Mnd1, 1.				
SQ	SEQUENCE 205 AA; 23753 MW; 95B0B14068DA0B51 CRC64;				

Query Match 100.0%; Score 1047; DB 2; Length 205;

Best Local Similarity 100.0%; Pred. No. 5.9e-56;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKGLSABEKRTRMEIFSETKDYFOLKDLKIAPEKIGITAMSVKEVLSQSLVDDGW 60
Db 1 MSKKGLSABEKRTRMEIFSETKDYFOLKDLKIAPEKIGITAMSVKEVLSQSLVDDGW 60

QY 61 DCEIRGTSNYWYAFPSKALHARKHKLTVLESQSLSEGSQKIASLQSIKAKIGRCETEE 120
Db 61 DCEIRGTSNYWYAFPSKALHARKHKLTVLESQSLSEGSQKIASLQSIKAKIGRCETEE 120

QY 121 TRLAKELSLRDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANRWTDNIFAIKSWA 180
Db 121 TRLAKELSLRDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANRWTDNIFAIKSWA 180

QY 181 KRKGFEEBKIDRTFGIPEDPDYID 205
Db 181 KRKGFEEBKIDRTFGIPEDPDYID 205

RESULT 2
Q8K396 PRELIMINARY; PRT; 205 AA.
AC 08K396;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-MAR-2004 (TREMBlrel. 22, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE GAW protein.
GN Name=2610034E18Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_Taxid=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshylyuk S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.D., Peters G.J., Abramson R.D., Muliahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield J.S.,
RA Krzywinski M.I., Skalka U., Smalhus D.E., Schmechel A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RA Strausberg R.L.; TISSUE=Mammary tumor;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027741; AAH27741.1;
DR MGD; MGI:1924165; 2610034E18Rik.
DR InterPro; IPRO05647; Mnd1.
DR Pfam; PF03962; Mnd1; 1.
SQ SEQUENCE 205 AA; 23849 MW; 122C3FA9E4325120 CRC64;

Query Match 91.4%; Score 954; DB 2; Length 205;
Best Local Similarity 89.8%; Pred. No. 2.5e-50;
Matches 184; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSKKGLSABEKRTRMEIFSETKDYFOLKDLKIAPEKIGITAMSVKEVLSQSLVDDGW 60

Db 1 MSKKGLSABEKRTRMEIFSETKDYFOLKDLKIAPEKIGITAMSVKEVLSQSLVDDGW 60

QY 61 DCEIRGTSNYWYAFPSKALHARKHKLTVLESQSLSEGSQKIASLQSIKAKIGRCETEE 120
Db 61 DCEIRGTSNYWYAFPSKALHARKHKLTVLESQSLSEGSQKIASLQSIKAKIGRCETEE 120

QY 121 TRLAKELSLRDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANRWTDNIFAIKSWA 180
Db 121 TRLAKELSLRDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANRWTDNIFAIKSWA 180

QY 181 KRKGFEEBKIDRTFGIPEDPDYID 205
Db 181 KRKGFEEBKIDRTFGIPEDPDYID 205

RESULT 3
Q9D0A1 PRELIMINARY; PRT; 205 AA.
AC Q9D0A1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA. RIKEN full-length
enriched library, clone:2610034E18 product:GAW homolog.
GN Name=2610034E18Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_Taxid=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The PANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtration of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,
RA Kono H., Akiyama Y., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format

RA	Fahney J., Helton B., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Roumhan J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywninski M.I., Skaleja U., Smalins D.E., Schnerch A., Schein J.F.,
RA	James S.J., Marra M.A.,
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[12]
RN	SEQUENCE FROM N.A.
RC	STRAIN=Singapore local strain; TISSUE=Embryo;
RA	Director MGC Project;
RA	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC078223; AAH78223.1; -.
DR	InterPro; IPR005647; Mnd1.
DR	InterPro; IPR005058; Wing_hlx_DNA_bnd.
DR	Pfam; PF03962; Mnd1; 1.
SQ	SEQUENCE 220 AA; 25176 MW; 90DEAA69311F4BF7 CRC64;
Query Match	61.5%; Score 644; DB 2; Length 220;
Best Local Similarity	71.8%; Pred. No. 1,4e-31;
Matches 125; Conservative	20; Mismatches 29; Indels 0; Gaps 0;
Oy	1 MSKKKGISABRRKRRMMEIFSETDVOVLKDLEIKAKRGITMSYKEVLOSIVDDGMV 60
Dd	1 MSKKKGISLBKRSMMEIFETDVOVLKDIEIKAKRSKITMSYKEVLOSIVDDNMV 60
Oy	61 DCEIGTSNYWAPPSALHARKHKLEVSQSSEGSOKHASLOKSIEKAKIGCETPEER 120
Dd	61 DTEVGTSNYWAPPSALHARKRKRLSELKQLSDGSRKALLQAADYKAVGRVNEER 120
Oy	121 TRLAKEISLRDREOLKAVEKYKCDPQVVEIRQANKVAKKANRWTDNIF 174
Dd	121 EDLKELTALKGQDKVKLEIKEQECDPAVVEIRANNTIAAKEVAVARMTGTGF 174
RESULT 5	
O86E28	PRELIMINARY; PRT; 196 AA.
O86E28	AC O86E28:
DT	01-JUN-2003 (Tremblrel. 24, Created)
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT	01-OCT-2003 (Tremblrel. 25, last annotation update)
DE	Clone ZSD1259 mRNA sequence.
OS	Schistosoma japonicum (Blood fluke).
CC	Eukaryote; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
CC	Schistosomatidae; Schistosomatidae; Schistosoma.
OX	NCBI_TaxID=6182;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
RX	Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
RA	Wang Z.J., Kong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
RA	Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
RA	Xue C.L., Feng Z., Chen Z., Han Z.G.,
RT	"Evolutionary and biomedical implications of a Schistosoma japonicum
RT	complementary DNA resource."
RL	Nat. Genet. 35:139-147(2003).
DR	EMBL; AY223066; AAP06089.1; -.
DR	InterPro; IPR005647; Mnd1.
DR	Pfam; PF03962; Mnd1; 1.
SQ	SEQUENCE 196 AA; 23163 MW; B30FEF08BD7123F0 CRC64;
Query Match	44.1%; Score 462; DB 2; Length 196;
Best Local Similarity	47.4%; Pred. No. 1.2e-20;
Matches 92; Conservative	34; Mismatches 68; Indels 0; Gaps 0;
Oy	11 EKTRRMEIFSSTDVFQOLKDLKIAKRGITAMSYKEVLOSIVDDGMDCERIGTSNY 70
Dd	2 KSRRMDPFYEKDFQOLKELRELCKEKGINSMRYKVLSLVHGVDVTDKIGTSYV 61
Oy	71 YWAFPSALHARKHKLEVSQSSEGSOKHASLOKSIEKAKIGCETPEERTRLAKEISL 130

```

Db      62 FMAFEPKAAQKLNKNIKVTGDIHTRNOIFKTRSLNELSKRKTEENRININTEL 121
      131 RDQRBLKAWEKCYKDCDPQVVEIRQANKVAKEANRWTDNIFAISNAKRGFEENK 190
      122 KILSELTLVLEQLEHGDHPDRLSLQQQLVLDNSANRWTDNIFVKSMLSNKFSIDEAT 181
Qy      191 IDRTFGIPEDFDYI 204
      182 FCRQFEIPENFDYI 195
RESULT 6
Q6G432 ID 08GYD2 PRELIMINARY; PRT; 230 AA.
AC 08GYD2;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein At4g29170/F19B15_200 (Hypothetical protein
DE At4g29170).
GN Name=At4g29170/F19B15_200; Synonyms=At4g29170;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eurosid 1; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hanan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shim P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK117113; BAC42364.1; -.
DR EMBL; BT005435; AA063855.1; -.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR005647; Mnd1.
DR Pfam; PF03962; Mnd1; 1.
KW Hypothetical protein.
SQ
SEQUENCE 230 AA; 26402 MW; 131BB5146D8C91ED CRC64;

Query Match 42.0%; Score 440; DB 2; Length 230;
Best Local Similarity 43.8%; Pred. No. 3,2e-19;
Matches 91; Conservative 43; Mismatches 70; Indels 4; Gaps 2;

Qy      1 MSKKKGLSAEKRTRMWEIFSTKDVFOLEKLIAPKEKGTAMSVKEVLQSLVDGMY 60
      1 MSKKRGSLSEKREKMLQIFYESQDFLLKELEKMGPK-KGVISQSVKDVIGSLVDDYLV 59
Db      61 DCEIRGTSNYWAFPSKALHARKHKEVLESQSGSKASLOKSIKAKIGRCETEE 120
      60 AKXKIGISLTFWSLPSCAGNQLRVSQKLESDDGSKRRLAEVLVDOCEALKGRRESER 119
Qy      121 TRLAKEISLRDQREOLKAWEKCYKDCDPQVVEIRQANKVAKEANRWTDNIFAISNA 180
      120 TRLATLQKLEKHKQLEKEMVQPADNDPATLEKRAIVAIQSANRWTDNIFTLRQNC 179
Qy      181 KRKFGFEENKIDRTF--GIPEDFDYI 205
      180 SNNFPQAKEQLEHMYTEAGITDEFDYIE 207
Db

```

```

Q6H432 ID 06H432 PRELIMINARY; PRT; 207 AA.
AC 06H432;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Putative GAI protein.
GN Name=P0651G05.20;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GAI) genomic DNA, chromosome 9, PAC
RT clone:P0651G05."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006528; BADD6517.1; -.
DR InterPro; IPR005647; Mnd1.
DR Pfam; PF03962; Mnd1; 1.
SQ
SEQUENCE 207 AA; 23900 MW; 6A9C5ECBBE6D586E CRC64;

Query Match 40.8%; Score 427; DB 2; Length 207;
Best Local Similarity 42.5%; Pred. No. 1.7e-18;
Matches 88; Conservative 44; Mismatches 71; Indels 4; Gaps 2;

Qy      1 MSKKKGLSAEKRTRMWEIFSTKDVFOLEKLIAPKEKGTAMSVKEVLQSLVDGMY 60
      1 MSKKRGSLSEKREKMLQIFYDSQDFYLLKELEKMGPK-KGVISQSVKDVIGSLVDDYLV 59
Db      61 DCEIRGTSNYWAFPSKALHARKHKEVLESQSGSKASLOKSIKAKIGRCETEE 120
      60 LKDKIGTSVTFWSLPSCAGNQLRTTYSKLESDDLSSKKRFLTEVQRENLKRGREDSER 119
Qy      121 TRLAKEISLRDQREOLKAWEKCYKDCDPQVVEIRQANKVAKEANRWTDNIFAISNA 180
      120 EALSELKAVEQEHKRLKEELAAVSDPALVANMDAIEVAHAANRWTDNIFTLQWC 179
Db      181 KRKFGFEENKID--RTFGIPEDFDYI 204
      180 STTFPQAKEQLEHMYREVIGITDEFDYIL 206
Qy      181 KRKFGFEENKID--RTFGIPEDFDYI 204
      180 STTFPQAKEQLEHMYREVIGITDEFDYIL 206
Db

```

```

RESULT 8
YA53 SCHPO STANDARD; PRT; 210 AA.
AC 009739;
DT 01-NOV-1995 (rel. 32, Created)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DT 05-JUL-2004 (rel. 44, Last annotation update)
DE Hypothetical protein C13A11.03 in chromosome 1.
GN ORFNames=SPAC13A11.03;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxId=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

```

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymoperez B.,
 RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leinrich H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambut R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forstburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe.",
 RL Nature 415:871-880(2002).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; 254096; CAA90804.1; -
 CC PIR; T37610; T37610
 CC DR GenBank; SPAC13A11.03; -
 CC DR InterPro; IPR005647; Mnd1.
 CC DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
 CC DR Pfam; PF03962; Mnd1; 1.
 CC DR Hypothetical protein.
 KW SEQUENCE 210 AA; 24224 MW; FA4546F070A37665 CRC64;
 SQ
 Query Match 33.3%; Score 349; DB 1; Length 210;
 Best Local Similarity 41.6%; Pred. No. 9e-14;
 Matches 84; Conservative 36; Mismatches 76; Indels 6; Gaps 5;
 QY 5 KGLSAEKKTRMMEIFSETKVDFOLKDLKIAPEKKGITAMSVKYLQSLVDGAVDCER 64
 DB 4 KGLSLAEKKRRLEAIFHDSKDFOLKEVEKLSK-KQIYLQIVYKQSLVDNIVKTEK 62
 QY 65 IGTSNYYAFPSKALHARKHKLVEESQSEGSOKHSLQSKI--EKAKIGRCETE-EKT 121
 DB 63 IGTSNYYAFPSKAKRSRESVLSLOAQDLDKQKSKTIDENISFKSKRGNDGETNDAN 122
 QY 122 RLAKELSLRD-QREOLKAVERKYKDCDPQVVEIRQANKVAKAANRTDNIFAIKSWA 180
 DB 123 QYTLBELHAKKESLKLKTQLSLNLHNCNPETPELKNENKTKWEANLMTDQHLTLAFC 182
 QY 181 KKKFGFEENKIDRTFGIPEDFD 202
 DB 183 -RDMGADTQIREYCSIPEDLD 203
 RESULT 9
 Q8SUA9 PRELIMINARY; PRT; 203 AA.
 AC 08SUA9;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Hypothetical protein ECU10_1600.
 GN Name=ECU10_1600;
 OS Encephalitozoon cuniculi GB-M1.
 OC Encephalitozoon cuniculi; Microsporidia; Unikaryonidae; Encephalitozoon.
 OX NCBI_TaxId=284813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
 RA Katinka M.D., Dupret S., Cornillot E., Metenier F., Thomarat F.,
 RA Premier G., Barde V., Peyretallade B., Brottier P., Winkler P.,

RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi.",
 RL Nature 414:450-453(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RA Genoscope;
 RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL590449; CAD25881.1; HPR_SerP_S.
 DR InterPro; IPR002114; HPR_SerP_S.
 DR InterPro; IPR005647; Mnd1.
 DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam; PF03962; Mnd1; 1.
 DR PROSITE; PS00589; Pts_HPR_SER; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 203 AA; 23743 MW; DPE33A65A1A28A42 CRC64;
 Query Match 32.5%; Score 340.5; DB 2; Length 203;
 Best Local Similarity 35.1%; Pred. No. 2.8e-13;
 Matches 71; Conservative 50; Mismatches 72; Indels 9; Gaps 3;
 QY 7 LSAEKKTRMMEIFSETKVDFOLKDLKIAPEKKGITAMSVKYLQSLVDGAVDCERIG 66
 DB 6 MKSDQKKSILHEIRIGSKSPFKQLQELSLGSK-KGIYVNTIKELIQQLVADGLVTAERKG 64
 QY 67 TSNYYAFPSKALHARKHKLVEESQSEGSOKHSLQSKI-EKAKIGRCETEERRLAKE 126
 DB 65 TSNLYSPASBSGIQKKLRCKELMEBCERMSQDICRKEKYLENEMSGHYEEERELBNK 124
 QY 127 LSSL-----RDREOLKAVERKYKDCDPQVVEIRQANKVAKAANRTDNIFAIKSWAKR 182
 DB 125 LWALKTKIQDQRE-----ELGKFEETDPIAYKLVADRKEMADENCRITIDNVIITIDYICS 180
 QY 183 KFGFEENKIDRTFGIPEDFDYI 204
 DB 181 KFPMEKSEFNSFGIPEDLDYI 202
 RESULT 10
 Q6MDA3 PRELIMINARY; PRT; 203 AA.
 AC 06MDA3;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Mnd1.
 OS Giardia lamblia (Giardia intestinalis).
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardiae; Giardia.
 OX NCBI_TaxId=57411;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ramesh M.A., Malik S.B., Logsdon J.M. Jr.;
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY295092; AAQ24512.1; -
 DR InterPro; IPR005647; Mnd1.
 DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam; PF03962; Mnd1; 1.
 SQ SEQUENCE 203 AA; 23278 MW; CC0625DCDC4158C0 CRC64;
 Query Match 32.5%; Score 340.5; DB 2; Length 203;
 Best Local Similarity 34.8%; Pred. No. 2.8e-13;
 Matches 70; Conservative 46; Mismatches 84; Indels 1; Gaps 1;
 QY 5 KGLSAEKKTRMMEIFSETKVDFOLKDLKIAPEKKGITAMSVKYLQSLVDGAVDCER 64
 DB 4 KGTSLDEKKERLEEMLRKGEIYSNKTITETLS-KPTGISSWIKVQLQALVNEDELVDYDK 62
 QY 65 IGTSNYYAFPSKALHARKHKLVEESQSEGSOKHSLQSKI-EKAKIGRCETEERTLA 124
 DB 63 IGASTYWCFCFSKRSQAARTELARQLALEBOTNFIIDATARIIEELKVGRETERSSLL 122

```
QY 125 KGLSLRDQEQKAEVEKYKDCDPQVEIRQANKVAKAANRWTDNIFAISMAKRF 184
DB 123 KETLALQVLEEQRGTFRDLLKNDPVAQKLRNYTDIAKQANLWTDNIFCLOKMYLTKL 182
QY 185 GFENKIDRTFGJPEDEYID 205
DB 183 QMDKTVSTALGTTGEFDYLE 203

RESULT 11
Q7QTX0 PRELIMINARY; PRT; 203 AA.
ID 07QTX0:
AC 07QTX0:
DB 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE GIP 76 12374 11763.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB0100100; EAA38463.1; -.
DR InterPro; IPR005647; Mnd1_hlx_DNA_bnd.
DR InterPro; IPR009058; Wln_hlx_DNA_bnd.
DR Pfam; PF03962; Mnd1; 1.
SQ SEQUENCE 203 AA; 23278 MW; CC0625DCDCA158C0 CRC64;

Query Match
Best Local Similarity 32.5%; Score 340.5; DB 2; Length 203;
Matches 70; Conservative 46; Mismatches 84; Indels 1; Gaps 1;

QY 5 KGLSAEKRTRMEIFSETKDVPOLKDLKIAPEKGIPTMSVKEVLSVDDGMDYDCR 64
DB 4 KGTSLDEKKEKRLLEMLKGEISNKTITLTS-KPTGISSMVKLVQALVNDVDVDTK 62
QY 65 IGTSNYYWAPPSPALHARKHLEVLSEQSSEGSQKASLSQKSIKAKIGCETEEETRLA 124
DB 63 IGASTYWCPSAKRSQAARTELARLQKALEEQTNFIDKATARIIEELKVGRETEERSILL 122
QY 125 KGLSLRDQEQKAEVEKYKDCDPQVEIRQANKVAKAANRWTDNIFAISMAKRF 184
DB 123 KETLALQVLEEQRGTFRDLLKNDPVAQKLRNYTDIAKQANLWTDNIFCLOKMYLTKL 182
QY 185 GFENKIDRTFGJPEDEYID 205
DB 183 QMDKTVSTALGTTGEFDYLE 203

RESULT 12
Q6Q9F9 PRELIMINARY; PRT; 179 AA.
ID 06Q9F9:
AC 06Q9F9:
DB 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE NMD1 domain containing protein.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
OX NCBI_TaxID=7153;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Chandra P.K., Wikel S.K.;
```

```
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY552061; AAS79347.1; -.
DR InterPro; IPR005647; Mnd1.
DR Pfam; PF03962; Mnd1; 1.
SQ SEQUENCE 179 AA; 20900 MW; 6E0016920350E476 CRC64;

Query Match
Best Local Similarity 31.8%; Score 332.5; DB 2; Length 179;
Matches 66; Conservative 52; Mismatches 57; Indels 3; Gaps 2;

QY 1 MSK-KKGLSAEKRTRMEIFSETKDVPOLKDLKIAPEKGIPTMSVKEVLSVDDGMDY 59
DB 1 MSK-KKGLSAEKRTRMEIFSETKDVPOLKDLKIAPEKGIPTMSVKEVLSVDDGMDY 59
QY 60 VDCERIGTSNYYWAPPSPALHARKHLEVLSEQSSEGSQKASLSQKSIKAKIGCETEE 119
DB 61 VETDIGSSQYVWFPAPKARKKXKQVFPOLKQEMEQSNDKIAELQKIGTIGESGESSR 120
QY 120 FRLAKELSLRDQEQKAEVE--KYDCDPQVEIRQANKVAKAANRWTDNIFA 175
DB 121 SSEMEFKLNTLKEKQKQLSSKLDKAKLKQSDQNSVDKNNRILPDILHDAANRWDTTYS 178

RESULT 13
Q7RH53 PRELIMINARY; PRT; 196 AA.
ID 07RH53:
AC 07RH53:
DB 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Homo sapiens GAD, putative.
GN Name=PY04140;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Koel T.W., Preece M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmiller S.B., Fieldlyum T.V.,
RA Cho J.K., Jaekenbush J., Sedegah M., Shoahbi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519 (2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01001237; EAA15959.1; -.
DR InterPro; IPR005647; Mnd1.
DR Pfam; PF03962; Mnd1; 1.
SQ SEQUENCE 196 AA; 23066 MW; 7FD8820707329074 CRC64;

Query Match
Best Local Similarity 26.5%; Score 277; DB 2; Length 196;
Matches 60; Conservative 52; Mismatches 76; Indels 14; Gaps 3;

QY 3 KKKGLSAEKRTRMEIFSETKDVPOLKDLKIAPEKGIPTMSVKEVLSVDDGMDYDC 62
DB 2 KKKGSNEDKRLIVDIMESEFFILKELELAAR-KKIRSIFKDLIQULIDNKTKS 60
QY 63 ERIGTSNYYWAPPSPALHARKHLEVLSEQSSEGSQKASLSQKSIKAKIGCETEE 115
DB 61 EKVGSONVFWILKTESSILQNKYQELDKDKEVEYEMQAKEENYALJENSLS-----L 114
QY 116 ETEERTLAKELSLRDQEQKAEVEKYKDCDPQVEIRQANKVAKAANRWTDNIFA 175
```

```

DB      115 KTDELKOTIKVEKYNVLDISEIKKSELDKLTCKTDIDRIQIEKMKIQSNFATESIERMNNIFL 174
QY      176 IKSNAKKRKGFEENKIDRTFGI 197
DB      175 LKQWITQDRTKNSGDVDRLLGM 196

```

RESULT 14

```

ID      06B0L5      PRELIMINARY;      PRT;      211 AA.
AC      06B0L5;
DT      25-OCT-2004 (TREMBlrel. 28, Created)
DT      25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT      25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE      Similar to CA3413|IPF9239 Candida albicans IPF9239 unknown function
       (fragment).
GN      ORFNames=DEHA0E04994g;
OS      Debaryomyces hanseali CBS767.
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX      NCBI_Taxid=284592;
RN      [1]
RC      SEQUENCE FROM N.A.
RP      STRAIN=CB8767;
RG      Genolevures;
RA      Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
       Latoucinie I., de Montigny J., Marck C., Neveglisse C., Talla E.,
       Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barde V.,
       Baray S., Blanchin S., Beckerich J.M., Beyne E., Bleykaesten C.,
       Boissarie A., Boyer J., Catolico L., Confantolieri F., de Daruvar A.,
       Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
       Hantraye F., Hemequin C., Jauniaux N., Joyet P., Kachouri R.,
       Kerrest A., Koszul R., Lemaire M., Lebur I., Ma L., Muller H.,
       Nicoud J.M., Nikolaki M., Otae S., Olier-Kalogeropoulos O.,
       Pellenn S., Peltier S., Richard G.F., Straub M.L., Suleau A.,
       Swenne D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
       Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
       RA      Bouchier C., Cauton B., Searpelli C., Gaillardin C., Weissenbach J.,
       Wincker P., Souciet J.L.;
       "Genome evolution in yeasts.";
       Nature 430:35-44(2004).
RT      Nature 430:35-44(2004).
RN      [2]
RC      SEQUENCE FROM N.A.
RP      STRAIN=CB8767;
RG      Genoscope;
RA      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; CR382137; CAG87731.1; -.
DR      InterPro; IPR005647; Mnd1.
PF      Pfam; PF03962; Mnd1; 1.
FT      NON_TER
SQ      SEQUENCE 211 AA; 24831 MW; F8B5D6C6618334C8 CRC64;

```

```

Query Match      25.5%; Score 266.5; DB 2; Length 211;
Best Local Similarity 29.0%; Pred. No. 8.8e-09;
Matches 61; Conservative 55; Mismatches 75; Indels 19; Gaps 5;

```

```

QY      4 KKGLSAEKRTKMEIFSETKDVFLQKLEKIAPKEKGTAMSVKVLQSLVDGMVDC 63
DB      3 KKGLSAEDKCKELVEFFNQSHFTYTLKEIKESGSKYAKISSMLKIDIVQQLIDMLNCE 62
QY      64 RIGTNSNYWAPPSKALHARKKLEVLVESQLS--EGSQKASLQKS--IEKATIGRCET-- 117
DB      63 KGGTNNLWYCF-----KFDKIKTLQTYNNYQNTLKEKOLERDOLIEKTLQGLQRLV 115
QY      118 ----BERTLAKELSLRDQREQLKAEVKEYKDCPQVEEIRQANKVAKAANRWTDNI 173
DB      116 KSDPGRNRLIDQFCLSKRKHLSEBLKAGDNDPQLIQTLDEKQVHLILAETFTDDI 175
QY      174 FAIKSWAKR--KFGFEENKIDRTFGIPEDF 201
DB      176 ESMIYFTKVSATIEBLDLRSELGIPSEF 205

```

```

RESULT 15
ID      075CH5      PRELIMINARY;      PRT;      225 AA.
AC      075CH5;
DT      05-JUL-2004 (TREMBlrel. 27, Created)
DT      05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE      ACL056CD.
GN      ORFNames=ACL056C;
OS      Ashbya gossypii (Yeast) (Bremothecium gossypii).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Bremothecium.
OX      NCBI_Taxid=33169;
RN      [1]
RC      SEQUENCE FROM N.A.
RP      STRAIN=ATCC 10895;
RA      Brachat S., Voegelé S.E., Dietrich F.S., Lerch A., Gaffney T.,
       Philippsen P.;
       Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AE016816; AAS51172.1; -.
DR      AGD; ACL056C; -.
DR      InterPro; IPR005647; Mnd1.
PF      Pfam; PF03962; Mnd1; 1.
SQ      SEQUENCE 225 AA; 25753 MW; BA73C889FFBEB90F CRC64;

```

```

Query Match      21.1%; Score 221; DB 2; Length 225;
Best Local Similarity 26.4%; Pred. No. 5.3e-06;
Matches 56; Conservative 51; Mismatches 93; Indels 12; Gaps 5;

```

```

QY      3 KKGLSAEKRTKMEIFSETKDVFLQKLEKIAPKE-KGITAMSVKVLQSLVDGMV 60
DB      4 KRAVYTLAEKARVILKFGQEHSHSTYSIDLEKLPKKAGVSNLWQVQLIDEDDLI 63
QY      61 DCERIGTNSNYWAPPSKALHARKKLEVLVESQLSEBSQKASLQKSIE-----KAKTGR 114
DB      64 SVEKGNVNVWCFNQVGVKQCTEMQMKARSESGVRLQELQAINSEKKHARAALFR 123
QY      115 CETERTT--LAKELSLRDQREQLKAEVKEYKDC--DPQVEEIRQANKVAKAANRW 170
DB      124 SEGVSYTRQALLTEHDELGRQLAALQSAVRYRLDPTKMDETKIDSYCRGVRSKLEQLDKIT 183
QY      171 DNFAIKSWAKRKGFEENKIDRTFGIPEDDP 202
DB      184 DNEIVYSFLMRRAVSRARLAAALDMPERE 215

```

```

Search completed: July 27, 2005, 09:40:57
Job time : 176 secs

```

~~BEST AVAILABLE COPY~~

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 09:29:49 ; Search time 42 Seconds
(without alignments)
364.359 Million cell updates/sec

Title: US-10-087-190-3

Perfect score: 1047
Sequence: 1 MSKKKGLSABEKRTIMEIF.....FEENKIDRTFGIPEDFDYID 205

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	593.5	56.7	127	4	US-09-621-976-4959 Sequence 4959, Ap
2	191.5	18.3	260	4	US-09-248-796A-14485 Sequence 14485, A
3	134.5	12.8	1270	4	US-09-538-092-1321 Sequence 1321, Ap
4	117	11.2	976	3	US-09-104-324B-4 Sequence 4, Appl
5	117	11.2	976	4	US-09-538-092-1339 Sequence 1339, Ap
6	114	10.9	284	4	US-09-914-259-55 Sequence 55, Appl
7	113.5	10.8	284	4	US-09-914-259-62 Sequence 62, Appl
8	112.5	10.7	630	4	US-09-248-796A-20275 Sequence 20275, A
9	112	10.7	284	4	US-09-914-259-43 Sequence 43, Appl
10	111	10.6	1337	4	US-09-538-092-918 Sequence 918, Appl
11	110	10.5	284	4	US-09-914-259-46 Sequence 46, Appl
12	110	10.5	284	4	US-09-914-259-49 Sequence 49, Appl
13	109.5	10.5	170	4	US-09-438-185A-708 Sequence 708, Appl
14	108	10.4	284	4	US-09-914-259-51 Sequence 51, Appl
15	108	10.3	817	4	US-09-248-796A-20276 Sequence 20276, A
16	107	10.2	281	4	US-09-914-259-63 Sequence 63, Appl
17	107	10.2	284	4	US-09-167-206-10 Sequence 10, Appl
18	107	10.2	284	4	US-09-914-259-40 Sequence 40, Appl
19	107	10.2	284	4	US-09-914-259-48 Sequence 48, Appl
20	107	10.2	284	4	US-09-914-259-50 Sequence 50, Appl
21	106.5	10.2	284	4	US-09-914-259-41 Sequence 41, Appl
22	106	10.1	534	4	US-09-103-664A-2 Sequence 2, Appl
23	106	10.1	1786	3	US-08-973-462-8 Sequence 8, Appl
24	105.5	10.1	224	2	US-08-772-255-16 Sequence 16, Appl
25	105.5	10.1	224	5	PCT-US95-08565-16 Sequence 16, Appl
26	105.5	10.1	245	4	US-10-164-595-34 Sequence 34, Appl
27	105	10.0	245	4	US-09-914-259-65 Sequence 65, Appl

28	105	10.0	251	4	US-09-914-259-64	Sequence 64, Appl
29	105	10.0	284	4	US-09-914-259-60	Sequence 60, Appl
30	104	9.9	1939	4	US-09-538-092-915	Sequence 915, Appl
31	104	9.9	1939	4	US-09-949-016-11104	Sequence 11104, A
32	102	9.7	281	4	US-09-914-259-45	Sequence 45, Appl
33	102	9.7	284	4	US-09-914-259-47	Sequence 47, Appl
34	102	9.7	284	4	US-09-914-259-57	Sequence 57, Appl
35	102	9.7	372	1	US-07-813-584A-3	Sequence 3, Appl
36	102	9.7	372	1	US-08-330-515-3	Sequence 3, Appl
37	102	9.7	1031	4	US-09-914-259-24	Sequence 24, Appl
38	102	9.7	1940	4	US-09-538-092-901	Sequence 901, Appl
39	102	9.7	1963	4	US-09-949-016-8888	Sequence 8888, Appl
40	101.5	9.7	2662	4	US-09-538-684B-31	Sequence 31, Appl
41	101.5	9.7	2663	4	US-09-538-092-1252	Sequence 1252, Appl
42	100.5	9.6	284	4	US-09-914-259-59	Sequence 59, Appl
43	100	9.6	1104	3	US-08-923-992A-4	Sequence 4, Appl
44	100	9.6	1164	3	US-08-923-992A-10	Sequence 10, Appl
45	99.5	9.5	588	4	US-08-714-741-42	Sequence 42, Appl

ALIGNMENTS

```
RESULT 1
US-09-621-976-4959
; Sequence 4959, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Maline Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSER.054PR2
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4959
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4959

Query Match      56.7% Score 593.5; DB 4; Length 127;
Best Local Similarity 89.6%; Pred. No. 1.7e-50;
Matches 120; Conservative 5; Mismatches 2; Indels 7; Gaps 1;

QY      1 MSKKKGLSABEKRTIMEIFSETKDVFLQKLEKIAPEKGTITANSYKVLQSLVDDGMV 60
      |||||
DB      1 MSKKKGLSABEKRTIMEIFSETKDVFLQKLEKIAPEKGTITANSYKVLQSLVDDGMV 60

QY      61 DCEKIGTNYWAFPSKALHARKKLEVLLESQLSGSGSHASLQSIKAKIGRCETTER 120
      |||||
DB      61 DCEKIGTNYWAFPSKALHARKKLEVLLESQLSGSGSHASLQSIKAKIGRCET--- 117

QY      121 TRLAKELSLNDOR 134
      |||||
DB      118 ----IKLSGMQDER 127

RESULT 2
US-09-248-796A-14485
; Sequence 14485, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.133
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
```

;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 14485
;; LENGTH: 260
;; TYPE: PRT
;; ORGANISM: Candida albicans
US-09-248-796A-14485

Query Match 18.3%; Score 191.5; DB 4; Length 260;
Best Local Similarity 27.1%; Pred. No. 8.8e-11;
Matches 59; Conservative 47; Mismatches 75; Indels 37; Gaps 8;

QY 1 MSKKGLSAEKKTRMMEIFSETKDVFLKDLKIAPKKGIATMSVKEVLQSLVDGAV 60
DB 60 MPKKGLTQEBKSLALINMFQSDHMFYTLKEISKASKQCKIPPMQKELVLAIVEGLV 119
QY 61 DCEKRTSNYYMAFPSPKALHARKHKEVLESQSGSKASQKSIKAK-----IGR 114
DB 120 EDRCGTLYLWSPF-----YLQHKQ-----QETHRLNRTIANLETERDSLICK 165
QY 115 C--ETERTFLAKELSLR-----DREQOLKAVEKVKDCDPQVVEIRQANKVAKAA 166
DB 166 CQDETGVNRQTHRAKIRPCDSLSERIDISQQLSKDSSES--VE-----NLVTSIAF 218
QY 167 NRTDNIIFAIKSWAKKRFGEENKIDRTFGIPEDFDYI 204
DB 219 --FSDSIDIDICYLRSQTGLTMTTLKTEFELPLFEFEI 254

RESULT 3
US-09-538-092-1321
; Sequence 1321, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1321
; LENGTH: 1270
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14203
US-09-538-092-1321

Query Match 12.8%; Score 134.5; DB 4; Length 1270;
Best Local Similarity 23.4%; Pred. No. 0.00028;
Matches 50; Conservative 43; Mismatches 106; Indels 15; Gaps 5;

QY 2 SKKGLSAEKKTRMMEIFSETKDVFLKDLKIAPKKGIATMSVKEVLQSLVDGAV 61
DB 271 ARKEAKEALEAKERYEMADTDADAIEMATLDKEMABEASLQOEVEALKEVDELTTD 330
QY 62 CERI-----GTSNYMAFPSPKALHAR-KHKEVLESQSGSKASQKSIKAK 110
DB 331 LELTKAEIEKSGDGAASVQLKQLEQNARKLDALVWRMDLSSSEKQEHVYKIQKMEK- 389
QY 111 KIGRCET--BERTFLAKELSLRDQREOLKAVEKVKDCDPQVVEIRQANKVAKAA 168
DB 390 KNOLELVNRQQRERLOEELSQAESTIDELKEQVDALGAE-EMVEMLTDRNLWLEEKVRE 448

QY 169 WTDNIFAIKSWAKKRFGEENKIDRTFGIPEDFD 202
DB 449 IRETVGDLEANNMENDLEQENARETELEIREQLD 482

RESULT 4
US-09-104-324B-4
; Sequence 4, Application US/09104324B
; Patent No. 6232460
; GENERAL INFORMATION:
; APPLICANT: T recit, Ozlem; Sahin, Ugur; Pfreundschuh, Michael
; TITLE OF INVENTION: Methods For Diagnosis And Treating Cancers,
; TITLE OF INVENTION: And Methods For Identifying Pathogenic Markers In A Sample Of
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,324B
FILING DATE: 25-June-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,702
FILING DATE: 15-July-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6232460man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5491
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-104-324B-4

Query Match 11.2%; Score 117; DB 3; Length 976;
Best Local Similarity 23.9%; Pred. No. 0.0099;
Matches 63; Conservative 38; Mismatches 85; Indels 78; Gaps 13;

QY 3 KKKGLSAE--KRTMMEL--FSETKDV-----FOLKDLKIAPKKGIATMSVKEVL 51
DB 413 QKKSSLEBMTKLTNNKEVELEELKVLGEKETLLYENKQFKIABELKG-TEQELIGLL 471
QY 52 QSL---VDDGAVDCERIGTSNYMAFPSPKAL-----HARKKLEYLE-- 90
DB 472 QAREKEVHLEIQLAITTSQGYSGKVDLKTLENEKLTNTETLSHCNKLSLENKELT 531
QY 91 -----SOLSGSQKASLQKSIKAKIGRCETETERRFLAKELSLRDQRE 136
DB 532 QETSDMTLELKNQOEDINNKKQOBERMLQIIE--NLQETETQLRNELEVRREELKQKDE 589
QY 137 LVAEVEKYD-CD-----POVVEIRQANKVAKS--AANRTDNIIFAIK----- 177
DB 590 VACKKDKSEBNCNNLRKQVENONKTIIEELQENKALKKGGTASQQLNVEIKVANKLE 649
QY 178 -SWAKKRFG-----FEENKI 191
DB 650 LSAKQKFGIITDYQKIEJDKKI 673

RESULT 5

```

US-09-538-092-1339
; Sequence 1339, Application US/09538092
; Patent No. 6753114
; GENERAL INFORMATION:
; APPLICANT: Glot, Lotic
; APPLICANT: Manfred, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1339
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q15431
US-09-538-092-1339

Query Match          11.2%; Score 117; DB 4; Length 976;
Best Local Similarity 23.9%; Pred. No. 0.0099;
Matches 63; Conservative 38; Mismatches 85; Indels 78; Gaps 13;

QY 3 KKKGSAE--KRTWMEI--FSETKOV-----FOLDLEKIAPEKGTAMSVKYL 51
DB 413 QKKSELEBMTKLTKNNKEVELKKVGEKSTLTYENKQFKIABELKG--TEQELIGL 471
QY 52 OSI---VDDGVDCRIGTSNYWAFPSKYL-----HARKHLEVL- 90
DB 472 QAREKEVDLEIQALITTSSEQYSGEVDLKTLENEKLTNTLSTHCKSLNKELT 531
QY 91 -----SOLSGSQKASLQKSTKAKIGRCETERTRLAKELSLDQEQ 136
DB 532 QETSDMTLELKNQOEINNNKQOEERMLKQIE--NIQETETQLRNELEVEEELKQKDE 589
QY 137 LKAEEVKYKD-CD-----POVEEIRQANKVAK- -AANRWTDNIFAK----- 177
DB 590 VACKLDKSENCNNLRKQVENKQKTIIELOQENKALKKGTASQOLNVTETKVNKLELE 649
QY 178 -SWAKRKTG-----FEENKI 191
DB 650 LESAKQKGEITDTYQKEIEDKKI 673

RESULT 6
US-09-914-259-55
; Sequence 55, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-914-259-55

Query Match          10.9%; Score 114; DB 4; Length 284;
Best Local Similarity 23.2%; Pred. No. 0.0037;

```

```

Matches 52; Conservative 37; Mismatches 61; Indels 74; Gaps 11;

QY 1 MSKKGSAE--EKRTWMEI--FSETKOVFOLDLEKIAPEKGTAMSVKLESLVDQ 57
DB 73 LAEKADADADVASLNRRIOLEBELDRAQ-----ERLA-----TALQKEAEKADDE 122
QY 58 ---GVDCERIGTSNYWAFPSKALHAR---KHLEVLSELSQSGSK----- 100
DB 123 SERGM-----KYIESRAQODEEMETQELQKEA--KHIAEDADRYE 163
QY 101 -----ASLQKSTKAKI--GRCETERTRLAKELSLDQEQKAEVEKYKCD 148
DB 164 EVARKLVIEESDLAEAEERAEISGKC-----AEIEBELKVTYNNLKSLEAQERYSQE 218
QY 149 POVEEIRQANKVAKAANRWTDNIFAKSMARKFGEENKID 192
DB 219 DKYEERIKVLSDKLEAEATR-----AEFAERSVTYKESID 254

RESULT 7
US-09-914-259-62
; Sequence 62, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-914-259-62

Query Match          10.8%; Score 113.5; DB 4; Length 284;
Best Local Similarity 21.1%; Pred. No. 0.0042;
Matches 48; Conservative 48; Mismatches 78; Indels 53; Gaps 8;

QY 2 SKKKLSA--EKKRTWMEI--FSETKOVFOLDLEKIAPEKGTAMSVK--EVLQSLVDGM 59
DB 45 AKKKLRASEDERDVLLELHKAEDSLAAD--ETAKAEADVASLNRRIOLEBELDRAQ 103
QY 60 VDCERIGTSNYWAFPSKALHARKHLEVLSELSQSGSK----- 99
DB 104 ---ERLATALQKLEAEAEKADSESGMKVIESRAQODEKVEIQEIQKAEKHIAEDADR 160
QY 100 -----HASLQKSTKAKI--GRCETERTRLAKELSLDQEQKAEVEKYK 145
DB 161 KYEEVARKLVIEESDLAEAEERAEISGKC-----AEIEBELKVTYNNLKSLEAQERYKS 215
QY 146 DCDPOVEEIRQANKVAKAANRWTDNIFAKSMARKFGEENKID 192
DB 216 QKEDYEERIKVLSDKLEAEATR-----AEFAERSVTYKESID 254

RESULT 8
US-09-248-796A-20275
; Sequence 20275, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13

```

```

; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20275
; LENGTH: 630
; TYPE: PRF
; ORGANISM: Candida albicans
US-09-248-796A-20275

```

```

Query Match          10.7%; Score 112.5; DB 4; Length 630;
Best Local Similarity 23.8%; Pred. No. 0.015;
Matches 49; Conservative 43; Mismatches 79; Indels 35; Gaps 8;

```

```

QY 3 KKKGLSAEKKRTMMEIFSETKOVFOLKDIETAPKEGITT-AMSVKEVLSQVDDGV 60
DB 158 KTKNSDTELKLEKQLELEKVK-----LDLOTADEKLKGTIEREIALKSELFTVKNSSG-- 210
QY 61 DCEKRTSNYYMFPS--KALHARKHKLTVL-----ESQSESGOKHSLQKSI----- 107
DB 211 ---LSTSELALTYTVKSLSEKEBELQPLSGNKSKELEDYIQKHSIDSEKULATDEL 266
QY 108 -EKAKIGRCETERTLAKELSLRDQEQKAEVEKYKCDPQVVEIRQANKVAKEA 166
DB 267 KERTKQFDSKSKKLTLENDLSTKKLELEKTKQTSKFNLEBKXKEIVKLNKELELK 326
QY 167 NRRTDNIFAIKSAKAKKFGFEENKID 192
DB 327 N---DN-----SGAKKELKVKSLB 344

```

```

RESULT 9
US-09-914-259-43
; Sequence 43, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 284
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-914-259-43

```

```

Query Match          10.7%; Score 112; DB 4; Length 284;
Best Local Similarity 23.5%; Pred. No. 0.0059;
Matches 52; Conservative 41; Mismatches 72; Indels 56; Gaps 9;

```

```

QY 1 MSKKGLSAEKK--RTRMMEIFSETKOVFQ-----LKDLEKAPK-EKGITAMSV 47
DB 73 LAEKKADAEAVASINRRIOVVEBELDRAQERLATALQLEBAEKVAADSEKGMKVIEN 132
QY 48 KEVLSQVDDGVDCERIGTSNYMFPSPKALHARKHKLTVLSQSESGOKHSLQKSI 107
DB 133 R---AKDEKKELEKLT-----OLKEAKHAEADKKEEVAARKVIIEGDL 176
QY 108 EKAKIGRCETERTRLA-----KELSSLRDQEQKAEVEKYKCDPQVVEIRQAN 159
DB 177 ER-----TEBAELAESKCSLEBELKVTNNLKSLEAQAKEYSQEKDYEEIKILT 229
QY 160 KVAKEAANRTDNIFAIKSAKAKKFGFEENKIDRTFGIPED 200
DB 230 DKLEKETRAE---FAERSVA-----KLKTIIDLD 258

```

```

RESULT 10
US-09-538-092-918

```

```

; Sequence 918, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Iolc
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqformatter Version 0.9
; SEQ ID NO 918
; LENGTH: 1937
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P13535
US-09-538-092-918

```

```

Query Match          10.6%; Score 111; DB 4; Length 1937;
Best Local Similarity 23.1%; Pred. No. 0.096;
Matches 54; Conservative 42; Mismatches 88; Indels 50; Gaps 9;

```

```

QY 4 KKKGLSAEKKRTMMEIFSETKOVFOLKDIETAPK-----EKGITAMS-----V 47
DB 1361 QPALSQANSEVQAQMTKTIETDAIQRTHELEAKKLAQRLQAEHVEAVNAKKSLEKT 1420
QY 48 KEVLSQVDDGVDCERIGTS-----NYMAFPKALHARKHKLTVLSQSESGQ 98
DB 1421 KQRLQNEVEDLMDLVDERSNAACAALDKKQRF-----DKVISEWQKQKBEQAELEASQK 1475
QY 99 KIASLOKSTIEKK-----IGRCET--BERTLAKELSLRDQ-----REQKAE 140
DB 1476 ESRSLSTELFKVKNYEEISLDLETLRRENKXLOOEISDLOIAEGGQIHLEKIKQ 1535
QY 141 VEKYDQDPQVVEIRQANKVAKEA-ANRWNTDNIFAIKSAKAKKFGFEENKIDR 193
DB 1536 VEOEK-CEIOALAEAEASLEHBEKILRIQLELVQVASEVDKIAEKDEEIDQ 1588

```

```

RESULT 11
US-09-914-259-46
; Sequence 46, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 284
; TYPE: PRF
; ORGANISM: Brachydanio rerio
US-09-914-259-46

```

```

Query Match          10.5%; Score 110; DB 4; Length 284;
Best Local Similarity 23.3%; Pred. No. 0.0092;
Matches 51; Conservative 44; Mismatches 72; Indels 52; Gaps 10;

```

```

QY 1 MSKKGLSAE---EKRTMMEIFSETKOVFQ-----LKDLEKAPK-EKGITAMSV 47
DB 73 LAEKKATDAEGDVASINRRIOVVEBELDRAQERLATALQLEBAEKVAADSEKGMKVIEN 132

```

```

OY      48 KEVQSLVDDGAVDCEBRTGTSYVWAFPSKJLHARKHKLVEVSQLSESSGOK-----HASTL 103
Db      133 R-----ALXDEBKEVMELOEI-----OLKEANHIAEEDRKYEEVARKLIVVEGEL 176

OY      104 OKSIEKAKI--GRCEETEERTRLAKELSSLDQREOLKAVEKEYKCDOPVVEIRQANKY 161
           :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      177 ERTEREAPLNBEGK-----SLEEBELKTYVTNMKSLLEQAEXKSKAKEDYEEBIEKVLTDK 231

OY      162 AKEAANRWTDNI FALKSWAKRKGFEENKIDRTFGIPEP 200
           |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      232 LKEAETRAE-----FAERSVA-----KLEKTIIDLED 258

RESULT 12
US-09-914-259-49
; Sequence 49, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Rana temporaria
; US-09-914-259-49.

```

```

Query Match      10.5%; Score 110; DB 4; Length 284;
Best Local Similarity 23.2%; Pred. No. 0.0092;
Matches 48; Conservative 39; Mismatches 80; Indels 40; Gaps 8

OY      1 MSKKKGISAE--EKRTTMEEIFSETKDFQ-----LXOLEKIAPK-EKGIITAMSV 47
          ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       73 LAEKKATPAADVADVSINRRIGQVEBELDRAQRRLATALQCKLEAEAKADESRGMKVIN 132
OY      48 KEVLQSLVDGWDVCERIGTSNYVAFPSKALHARKGLVLESQSSEGSQHASIQSKI 107
          :.:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       133 R----ALDXEEIKELQEI-----QLKEAKHIAEBADRKYEEFARLVIIIEGDL 176
OY      108 EKAKIGRETBER--TRLAKETSLARDQROUKADEVKRYKDDPQVVERIRQANKAYKA 165
          ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       177 ERAE-ERALESBSKCAELEBELKTVTNNLKLSLEAQEKYSQKEDXEI KVLTDKLKEA 235
OY      166 ANRWTDNIFAISKWARRKFGEENKID 192
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       236 ETR-----AEFAERTVAKLKESID 254
          :.:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 13
US-09-438-185A-708
Sequence 708. Application US/09438185A
Patent No. 6822071
GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT FILING DATE: US/09/438,185A
PRIOR APPLICATION NUMBER: 2002-03-13
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1999-04-08
```

```

: NUMBER OF SEQ ID NOS: 1074
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 708
: LENGTH: 170
: TYPE: PRT
: ORGANISM: Chlamydia pneumoniae
: FEATURE:
: OTHER INFORMATION: CPn0706
: US-09-458-185A-708

Query Match          10.5%; Score 109.5; DB 4; Length 170;
Best Local Similarity 29.8%; Pred. No. 0.0052;
Matches 48; Conservative 29; Mismatches 51; Indels 33; Gaps 8;

```

```
OY      1 EERKTAMEIIFSETXDVQLKDLKELAKRKGITAMVEIGTSLVDGHWDCVERIGTSN 69
          :|::||::||::||::||::||::||::||::||::||::||::||::||:
Db      27 KEKR-RILTEBO-----KLREKEARDKXKNHMQIKQ-LRIPLDEGT-----   70

OY      70 YWAFPSKLIARKHLEVLLESOLSE-----GSQKHAL--OKSIEKATIG--RCETES 119
          :|::||::||::||::||::||::||::||::||::||::||::||:
Db      71 -----SDAVLOKSIIKYVAVOLSEBEKKNNKOEVLAASKLELQABNLAKRKREE 124

OY      120 RTFLAKEISLRDORQLKAEEVKCDPDPVEIEIRQANK 160
          :|::||::||::||::||::||::||::||::||::||::||::||:
Db      125 KTRLHKHEEMKALKEBARAB-EKQDMGOLLVOLQOKK 164
```

```

RESULT 14
US-09-914-259--51
: Sequence 51: Application US/09914259
: Patent No. 6495336
: GENERAL INFORMATION:
: APPLICANT: Makowski, Lee
: APPLICANT: Hyman, Paul
: APPLICANT: Williams, Mark
: TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
: FILE REFERENCE: 8471-010-999
: CURRENT APPLICATION NUMBER: US/09/914,259
: CURRENT FILING DATE: 2000-11-21
: NUMBER OF SEQ ID NOS: 180
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 51
: LENGTH: 264
: TYPE: PRT
: ORGANISM: Xenopus laevis
US-09-914-259--51

```

	Query Match	10.4%; Score 109; DB 4;
	Best Local Similarity	23.7%; Pred. No. 0.011;
	Matches	49; Conservative 37; Mismatches 81; Indels 40; Gaps 8
Qy	1 MSKKKGLSAAE--EKRTMMEIFSETKYDFVQ-----LKDLKTAAPK-EKGITAMSV 47	
Db	73 LSDKCATDAEDGVALNRRIQLVEEEELDPAQRSLTALQLEAEAKADESEERGMKIYEN 132	
Qy	48 KEVQSLVDGDMDVCERIGTSNYTWAFPSKLHARKLTVLBLEOSLSGSGKHASLOKSI 107	
Db	133 R---ALKDESKMLQET-----OLKEAKHIAESADRYEEVAARLVIIISDL 176	
Qy	108 EKATIGRCETEER--TRLAKELSSLRDQEQLTAKVEKYKDQDPQVVEIRQANKVAXEA 165	
Db	177 ERAAEIKAEIASESKCAIEBELKVTIVNNLKSLELAQAERYSQCKEDRYEIEIKVLDTLKEA 235	
Qy	166 ANRPTDNIFAIKSWAKRKFGPEENKID 192	
Db	236 ETR-----AAFEARTVAKLESID 254	

RESULT 15
US-09-248-796A-20276
; Sequence 20276, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 09:41:05 ; Search time 156 Seconds
(without alignments)
511.176 Million cell updates/sec

Title: US-10-087-190-3
Perfect score: 1047
Sequence: 1 MSKKKGLAEKRTMWEIF.....FENKIDRTFGIPEDFYID 205

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047	100.0	205	10	US-09-799-250-2
2	1047	100.0	205	15	US-10-087-190-3
3	1047	100.0	205	15	US-10-087-190-14
4	1047	100.0	205	15	US-10-087-190-20
5	1047	100.0	205	15	US-10-087-190-21
6	1047	100.0	205	15	US-10-087-190-22
7	1047	100.0	205	15	US-10-087-190-61
8	1047	100.0	205	16	US-10-408-765A-1821
9	1036.5	99.0	206	15	US-10-087-190-44
10	1036.5	99.0	206	15	US-10-087-190-45
11	1011	96.6	198	15	US-10-087-190-24

12	975	93.1	190	15	US-10-087-190-13	Sequence 13, Appl
13	975	93.1	190	15	US-10-087-190-19	Sequence 19, Appl
14	975	93.1	190	15	US-10-087-190-67	Sequence 67, Appl
15	975	93.1	190	15	US-10-087-190-68	Sequence 68, Appl
16	975	93.1	190	15	US-10-087-190-69	Sequence 69, Appl
17	948	90.5	205	15	US-09-799-250-4	Sequence 4, Appl1
18	948	90.5	205	15	US-10-087-190-23	Sequence 23, Appl
19	945.5	90.3	190	15	US-10-087-190-11	Sequence 11, Appl
20	945.5	90.3	190	15	US-10-087-190-18	Sequence 18, Appl
21	945.5	90.3	190	15	US-10-087-190-62	Sequence 62, Appl
22	945.5	90.3	190	15	US-10-087-190-63	Sequence 63, Appl
23	614	58.6	122	15	US-10-087-190-53	Sequence 53, Appl
24	591	56.4	122	15	US-10-087-190-9	Sequence 9, Appl1
25	591	56.4	122	15	US-10-087-190-57	Sequence 57, Appl
26	591	56.4	122	15	US-10-087-190-54	Sequence 54, Appl
27	591	56.4	122	15	US-10-087-190-55	Sequence 55, Appl
28	584	55.8	119	15	US-10-087-190-7	Sequence 7, Appl1
29	584	55.8	119	15	US-10-087-190-16	Sequence 16, Appl
30	584	55.8	119	15	US-10-087-190-47	Sequence 47, Appl
31	465	44.4	126	15	US-10-087-190-5	Sequence 5, Appl1
32	465	44.4	126	15	US-10-087-190-15	Sequence 15, Appl
33	465	44.4	126	15	US-10-087-190-46	Sequence 46, Appl
34	434	41.5	207	16	US-10-425-115-253013	Sequence 253013,
35	427	40.8	207	16	US-10-437-963-162899	Sequence 162899,
36	394	37.6	235	16	US-10-437-963-162901	Sequence 162901,
37	349	33.3	200	10	US-09-799-250-5	Sequence 5, Appl1
38	349	33.3	200	15	US-10-087-190-25	Sequence 25, Appl
39	287	27.4	79	14	US-10-106-698-5443	Sequence 5443, Ap
40	255.5	24.4	218	14	US-10-083-357-1304	Sequence 1304, Ap
41	214.5	20.5	74	15	US-10-424-599-192650	Sequence 192650,
42	121.5	11.6	715	16	US-10-408-765A-2096	Sequence 2096, Ap
43	121.5	11.6	1881	14	US-10-032-585-7646	Sequence 7646, Ap
44	120.5	11.5	1798	10	US-09-981-151A-48	Sequence 48, Appl
45	120	11.5	882	17	US-10-732-923-3300	Sequence 3300, Ap

ALIGNMENTS

RESULT 1
US-09-799-250-2
; Sequence 2, Application US/09799250
; Publication No. US20030032087A1
GENERAL INFORMATION:
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.34US01
; CURRENT APPLICATION NUMBER: US/09/799,250
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250-2
Query Match 100.0%; Score 1047; DB 10; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKKGLAEKRTMWEIFSETKDVFLKLEKAPREKGTANSYKVLQSLVDENV 60
DB 1 MSKKKGLAEKRTMWEIFSETKDVFLKLEKAPREKGTANSYKVLQSLVDENV 60
QY 61 DCRIGTSNYWAFPSKALHARKHKLVLSEQLSEGSQKHSALQSIKAKIGRCETBE 120

```
Db      61 DCRIGTSNYVAFPSKALHARKHKLVELESQSLSESGQKASLQKSIERAKIGRCETER 120
        |||||
Qy      121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRMTDNIFAIKSMA 180
        |||||
Db      121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRMTDNIFAIKSMA 180
        |||||
Qy      181 KRKFGFEENKIDRTFGIPEDFDYID 205
        |||||
Db      181 KRKFGFEENKIDRTFGIPEDFDYID 205
        |||||
```

RESULT 2

```
US-10-087-190-3
; Sequence 3, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-3
```

```
Query Match      100.0%; Score 1047; DB 15; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MSKKGSLAEKRTMEIFSETKDVFOQLKLEKIAPKEKGTAMSVEKVLQSLVDGMY 60
        |||||
Db      1 MSKKGSLAEKRTMEIFSETKDVFOQLKLEKIAPKEKGTAMSVEKVLQSLVDGMY 60
        |||||
Qy      61 DCRIGTSNYVAFPSKALHARKHKLVELESQSLSESGQKASLQKSIERAKIGRCETER 120
        |||||
Db      61 DCRIGTSNYVAFPSKALHARKHKLVELESQSLSESGQKASLQKSIERAKIGRCETER 120
        |||||
Qy      121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRMTDNIFAIKSMA 180
        |||||
Db      121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRMTDNIFAIKSMA 180
        |||||
Qy      181 KRKFGFEENKIDRTFGIPEDFDYID 205
        |||||
Db      181 KRKFGFEENKIDRTFGIPEDFDYID 205
        |||||
```

RESULT 3

```
US-10-087-190-14
; Sequence 14, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
```

```
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-14
```

```
Query Match      100.0%; Score 1047; DB 15; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MSKKGSLAEKRTMEIFSETKDVFOQLKLEKIAPKEKGTAMSVEKVLQSLVDGMY 60
        |||||
Db      1 MSKKGSLAEKRTMEIFSETKDVFOQLKLEKIAPKEKGTAMSVEKVLQSLVDGMY 60
        |||||
Qy      61 DCRIGTSNYVAFPSKALHARKHKLVELESQSLSESGQKASLQKSIERAKIGRCETER 120
        |||||
Db      61 DCRIGTSNYVAFPSKALHARKHKLVELESQSLSESGQKASLQKSIERAKIGRCETER 120
        |||||
Qy      121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRMTDNIFAIKSMA 180
        |||||
Db      121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRMTDNIFAIKSMA 180
        |||||
Qy      181 KRKFGFEENKIDRTFGIPEDFDYID 205
        |||||
Db      181 KRKFGFEENKIDRTFGIPEDFDYID 205
        |||||
```

RESULT 4

```
US-10-087-190-20
; Sequence 20, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-20
```

```
Query Match      100.0%; Score 1047; DB 15; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MSKKGSLAEKRTMEIFSETKDVFOQLKLEKIAPKEKGTAMSVEKVLQSLVDGMY 60
        |||||
Db      1 MSKKGSLAEKRTMEIFSETKDVFOQLKLEKIAPKEKGTAMSVEKVLQSLVDGMY 60
        |||||
```

Qy 61 DCRIGTSNYWAFPSKALHARKHLEVLSELSQSGSHASLOKSIKAKIGRCETEE 120
Db 61 DCRIGTSNYWAFPSKALHARKHLEVLSELSQSGSHASLOKSIKAKIGRCETEE 120
Qy 121 TRLAEISLSDRQRLKAEVEKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 180
Db 121 TRLAEISLSDRQRLKAEVEKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 180
Qy 181 KRKFGFEENKIDRTFGIPEDFDYID 205
Db 181 KRKFGFEENKIDRTFGIPEDFDYID 205

RESULT 5
US-10-087-190-21
Sequence 21, Application US/10087190
Publication No. US2003022397A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P11 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-21

Query Match 100.0%; Score 1047; DB 15; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSKKKGLSAEKRTTMEIFSETKDVFLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
Db 1 MSKKKGLSAEKRTTMEIFSETKDVFLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
Qy 61 DCRIGTSNYWAFPSKALHARKHLEVLSELSQSGSHASLOKSIKAKIGRCETEE 120
Db 61 DCRIGTSNYWAFPSKALHARKHLEVLSELSQSGSHASLOKSIKAKIGRCETEE 120
Qy 121 TRLAEISLSDRQRLKAEVEKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 180
Db 121 TRLAEISLSDRQRLKAEVEKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 180
Qy 181 KRKFGFEENKIDRTFGIPEDFDYID 205
Db 181 KRKFGFEENKIDRTFGIPEDFDYID 205

RESULT 6
US-10-087-190-22
Sequence 22, Application US/10087190
Publication No. US2003022397A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Afar, Daniel E. H.

APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P11 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-22

Query Match 100.0%; Score 1047; DB 15; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSKKKGLSAEKRTTMEIFSETKDVFLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
Db 1 MSKKKGLSAEKRTTMEIFSETKDVFLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
Qy 61 DCRIGTSNYWAFPSKALHARKHLEVLSELSQSGSHASLOKSIKAKIGRCETEE 120
Db 61 DCRIGTSNYWAFPSKALHARKHLEVLSELSQSGSHASLOKSIKAKIGRCETEE 120
Qy 121 TRLAEISLSDRQRLKAEVEKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 180
Db 121 TRLAEISLSDRQRLKAEVEKYDCDPQVVEIRQANKVAKAANRWTDNIFAIKSWA 180
Qy 181 KRKFGFEENKIDRTFGIPEDFDYID 205
Db 181 KRKFGFEENKIDRTFGIPEDFDYID 205

RESULT 7
US-10-087-190-61
Sequence 61, Application US/10087190
Publication No. US2003022397A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P11 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 61
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-61

Query Match 100.0%; Score 1047; DB 15; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSKKKGLSAEKRTTMEIFSETKDVFLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
Db 1 MSKKKGLSAEKRTTMEIFSETKDVFLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60

```
QY 61 DCRIGTSNYWAFPSKALHARKHKLVLVSQLSGSGOKHSLQKSIIEKAKIGRCETEE 120
| | | | |
DB 61 DCRIGTSNYWAFPSKALHARKHKLVLVSQLSGSGOKHSLQKSIIEKAKIGRCETEE 120
QY 121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAISMA 180
| | | | |
DB 121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAISMA 180
QY 181 KRRKGFEEENKIDRTFGIPEDFDYID 205
| | | | |
DB 181 KRRKGFEEENKIDRTFGIPEDFDYID 205

RESULT 8
US-10-408-765A-1821
; Sequence 1821, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bo D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088, 465
; CURRENT APPLICATION NUMBER: US/10/408, 765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1821
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1821

Query Match 100.0%; Score 1047; DB 16; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEKKRTMMEIFSETKDFVFLKDLKIAPEKGITAMSVKEVLQSLVDDGV 60
| | | | |
DB 1 MSKKKGLSAEKKRTMMEIFSETKDFVFLKDLKIAPEKGITAMSVKEVLQSLVDDGV 60
QY 61 DCRIGTSNYWAFPSKALHARKHKLVLVSQLSGSGOKHSLQKSIIEKAKIGRCETEE 120
| | | | |
DB 61 DCRIGTSNYWAFPSKALHARKHKLVLVSQLSGSGOKHSLQKSIIEKAKIGRCETEE 120
QY 121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAISMA 180
| | | | |
DB 121 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAISMA 180
QY 181 KRRKGFEEENKIDRTFGIPEDFDYID 205
| | | | |
DB 181 KRRKGFEEENKIDRTFGIPEDFDYID 205

RESULT 9
US-10-087-190-44
; Sequence 44, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afari, Daniel E. H.
; APPLICANT: Ge, Wengmao
; APPLICANT: Jakobovitz, Aya
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-44

Query Match 99.0%; Score 1036.5; DB 15; Length 206;
Best Local Similarity 99.5%; Pred. No. 2.8e-77;
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSKKKGLSAEKKRTMMEIFSETKDFVFLKDLKIAPEKGITAMSVKEVLQSLVDDGV 60
| | | | |
DB 1 MSKKKGLSAEKKRTMMEIFSETKDFVFLKDLKIAPEKGITAMSVKEVLQSLVDDGV 60
QY 61 DCRIGTSNYWAFPSKALHARKHKLVLVSQLSGSGOKHSLQKSIIEKAKIGRCETEE 119
| | | | |
DB 61 DCRIGTSNYWAFPSKALHARKHKLVLVSQLSGSGOKHSLQKSIIEKAKIGRCETEE 120
QY 120 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAISMA 179
| | | | |
DB 120 TRLAKELSLRDQREOLKAVEKYKDCDPQVVEIRQANKVAKAANRWTDNIFAISMA 180
QY 180 AKRKGFEENKIDRTFGIPEDFDYID 205
| | | | |
DB 180 AKRKGFEENKIDRTFGIPEDFDYID 206

RESULT 10
US-10-087-190-45
; Sequence 45, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afari, Daniel E. H.
; APPLICANT: Ge, Wengmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-45

Query Match 99.0%; Score 1036.5; DB 15; Length 206;
Best Local Similarity 99.5%; Pred. No. 2.8e-77;
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSKKKGLSAEKKRTMMEIFSETKDFVFLKDLKIAPEKGITAMSVKEVLQSLVDDGV 60
| | | | |
DB 1 MSKKKGLSAEKKRTMMEIFSETKDFVFLKDLKIAPEKGITAMSVKEVLQSLVDDGV 60
QY 61 DCRIGTSNYWAFPSKALHARKHKLVLVSQLSGSGOKHSLQKSIIEKAKIGRCETEE 119
```

```
Db 61 DCEIGTSNYWAFPSKALHARKHLEVESOLESEGSOKHASLOKSIERAKIGRCETEE 120
QY 120 RRLAKESLSDOREQKAEVEKYKDCDPQVEEIRQANKVAKAANRWTDNIFAISW 179
Db 121 RRLAKESLSDOREQKAEVEKYKDCDPQVEEIRQANKVAKAANRWTDNIFAISW 180
QY 180 AKRKGFEENKIDRTFGIPEDFDYID 205
Db 181 AKRKGFEENKIDRTFGIPEDFDYID 206

RESULT 11
US-10-087-190-24
; Sequence 24, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Jakobovitz, Aya
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-24

Query Match 96.6%; Score 1011; DB 15; Length 198;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KLSAEKRTMWEIFSEKDVPOKLEKIPKKEGITAMSVKYLQSLVDDGAVDCER 64
Db 1 KLSAEKRTMWEIFSEKDVPOKLEKIPKKEGITAMSVKYLQSLVDDGAVDCER 60
QY 65 IGTSNYWAFPSKALHARKHLEVESOLESEGSOKHASLOKSIERAKIGRCETERTLA 124
Db 61 IGTSNYWAFPSKALHARKHLEVESOLESEGSOKHASLOKSIERAKIGRCETERTLA 120
QY 125 KLSLSDOREQKAEVEKYKDCDPQVEEIRQANKVAKAANRWTDNIFAISWAKRKF 184
Db 121 KLSLSDOREQKAEVEKYKDCDPQVEEIRQANKVAKAANRWTDNIFAISWAKRKF 180
QY 185 GFEENKIDRTFGIPEDFD 202
Db 181 GFEENKIDRTFGIPEDFD 198

RESULT 12
US-10-087-190-13
; Sequence 13, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
```

```
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-13

Query Match 93.1%; Score 975; DB 15; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.9e-72;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MWEIFSEKDVPOKLEKIPKKEGITAMSVKYLQSLVDDGAVDCERIGTSNYWAF 75
Db 1 MWEIFSEKDVPOKLEKIPKKEGITAMSVKYLQSLVDDGAVDCERIGTSNYWAF 60
QY 76 SKALHARKHLEVESOLESEGSOKHASLOKSIERAKIGRCETERTERTLAKEISLSDORE 135
Db 61 SKALHARKHLEVESOLESEGSOKHASLOKSIERAKIGRCETERTERTLAKEISLSDORE 120
QY 136 QKAEVEKYKDCDPQVEEIRQANKVAKAANRWTDNIFAISWAKRKGFEENKIDRTF 195
Db 121 QKAEVEKYKDCDPQVEEIRQANKVAKAANRWTDNIFAISWAKRKGFEENKIDRTF 180
QY 196 GIPEDFDYID 205
Db 181 GIPEDFDYID 190

RESULT 13
US-10-087-190-19
; Sequence 19, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-19

Query Match 93.1%; Score 975; DB 15; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.9e-72;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MWEIFSEKDVPOKLEKIPKKEGITAMSVKYLQSLVDDGAVDCERIGTSNYWAF 75
Db 1 MWEIFSEKDVPOKLEKIPKKEGITAMSVKYLQSLVDDGAVDCERIGTSNYWAF 60
```

Qy	7	STALHARKKLEVL	ESQ	SEGSQKIA	SLQKSLERKAKICRCETERTRLAKELSLAPORE	135
Db	61	STALHARKKLEVL	ESQ	SEGSQKIASLQKSLERKAKICRCETERTRLAKELSLAPORE	130	
Qy	136	QKABEYKXKDD	POVEI	IRQANVAKKANRWTDNI	FAIKSNAXKPFGEENKIDRTF	195
Db	121	QKABEYKXKDD	POVEI	IRQANVAKKANRWTDNIFAIKSNAXKPFGEENKIDRTF	180	
Qy	196	GIPEDFDYID	205			
Db	181	GIPEDFDYID	190			

```

RESTLT 14      US-10-087-190-67
; Sequence 67, Application US/10087190
; Publication NO. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Fatis, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-087-190-67

```

```

APPLICANT: Ge, Mangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
PRIOR FILING DATE: 2003-01-28
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68
LENGTH: 190
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-68

Query Match 93.1%; Score 975; DB 15; Length 190;
Best Local Similarity 100.0%; Pred. 2.9e-72;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MMEIFSTKGVFOIKDLKTAPEKKGKTAMVKEVLOSIVDGDWDCERIGTSNYMAFP 75
Db 1 MMEIFSTKGVFOIKDLKTAPEKKGKTAMVKEVLOSIVDGDWDCERIGTSNYMAFP 60
QY 76 SKALHARKHKLKLEVLSEQLSEGSQGHASLQKSIIEKAKIGRCETERTLAKELSLRDQRE 135
Db 61 SKALHARKHKLKLEVLSEQLSEGSQGHASLQKSIIEKAKIGRCETERTLAKELSLRDQRE 120
QY 136 QLKAEVEKYKCDPQVYVEIRQANKVAKAANRWTDNIFAIKSNAKRKGFPEENKIDRTF 195
Db 121 QLKAEVEKYKCDPQVYVEIRQANKVAKAANRWTDNIFAIKSNAKRKGFPEENKIDRTF 180
QY 196 GIPEDFDYID 205
Db 181 GIPEDFDYID 190

```

Search completed: July 27, 2005, 09:54:35
Job time : 157 secs

RESULT 15
US-10-087-190-68
Sequence 68, Application US/10067190
Publication No. US2003023297A1
GENERAL INFORMATION:
APPLICANT: Agencys, Inc.
APPLICANT: Challita-Rld, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Ralcato, Arthur B.
APPLICANT: Fairs, Mary
APPLICANT: Afar, Daniel E. H.